FIG. 1A-1

(SEQ ID NO:1)

```
          11          20          29          38          47          56
5'  GAG ACT CAC GGT CAA GCT AAG GCG AAG AGT GGG TGG CTG AAG CCA TAC TAT TTT
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---

          65          74          83          92          101         110
    ATA GAA TTA ATG GAA AGC AGA AAA GAC ATC ACA AAC CAA GAA GAA CTT TGG AAA
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
(SEQ ID NO:2)→ M   E   S   R   K   D   I   T   N   Q   E   E   L   W   K

          119         128         137         146         155         164
    ATG AAG CCT AGG AGA AAT TTA GAA GAA GAC GAT TAT TTG CAT AAG GAC ACG GGA
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     M   K   P   R   R   N   L   E   E   D   D   Y   L   H   K   D   T   G

          173         182         191         200         209         218
    GAG ACC AGC ATG CTA AAA AGA CCT GTG CTT TTG CAT TTG CAC CAA ACA GCC CAT
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     E   T   S   M   L   K   R   P   V   L   L   H   L   H   Q   T   A   H

          227         236         245         254         263         272
    GCT GAT GAA TTT GAC TGC CCT TCA GAA CTT CAG CAC ACA CAG GAA CTC TTT CCA
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     A   D   E   F   D   C   P   S   E   L   Q   H   T   Q   E   L   F   P

          281         290         299         308         317         326
    CAG TGG CAC TTG CCA ATT AAA ATA GCT GCT ATT ATA GCA TCT CTG ACT TTT CTT
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     Q   W   H   L   P   I   K   I   A   A   I   I   A   S   L   T   F   L

          335         344         353         362         371         380
    TAC ACT CTT CTG AGG GAA GTA ATT CAC CCT TTA GCA ACT TCC CAT CAA CAA TAT
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     Y   T   L   L   R   E   V   I   H   P   L   A   T   S   H   Q   Q   Y

          389         398         407         416         425         434
    TTT TAT AAA ATT CCA ATC CTG GTC ATC AAC AAA GTC TTG CCA ATG GTT TCC ATC
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     F   Y   K   I   P   I   L   V   I   N   K   V   L   P   M   V   S   I

          443         452         461         470         479         488
    ACT CTC TTG GCA TTG GTT TAC CTG CCA GGT GTG ATA GCA GCA ATT GTC CAA CTT
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     T   L   L   A   L   V   Y   L   P   G   V   I   A   A   I   V   Q   L

          497         506         515         524         533         542
    CAT AAT GGA ACC AAG TAT AAG AAG TTT CCA CAT TGG TTG GAT AAG TGG ATG TTA
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     H   N   G   T   K   Y   K   K   F   P   H   W   L   D   K   W   M   L

          551         560         569         578         587         596
    ACA AGA AAG CAG TTT GGG CTT CTC AGT TTC TTT TTT GCT GTA CTG CAT GCA ATT
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     T   R   K   Q   F   G   L   L   S   F   F   F   A   V   L   H   A   I

          605         614         623         632         641         650
    TAT AGT CTG TCT TAC CCA ATG AGG CGA TCC TAC AGA TAC AAG TTG CTA AAC TGG
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     Y   S   L   S   Y   P   M   R   R   S   Y   R   Y   K   L   L   N   W
```

FIG. 1A-2

```
          659        668        677        686        695        704
GCA TAT CAA CAG GTC CAA CAA AAT AAA GAA GAT GCC TGG ATT GAG CAT GAT GTT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 A   Y   Q   Q   V   Q   Q   N   K   E   D   A   W   I   E   H   D   V

          713        722        731        740        749        758
TGG AGA ATG GAG ATT TAT GTG TCT CTG GGA ATT GTG GGA TTG GCA ATA CTG GCT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 W   R   M   E   I   Y   V   S   L   G   I   V   G   L   A   I   L   A

          767        776        785        794        803        812
CTG TTG GCT GTG ACA TCT ATT CCA TCT GTG AGT GAC TCT TTG ACA TGG AGA GAA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 L   L   A   V   T   S   I   P   S   V   S   D   S   L   T   W   R   E

          821        830        839        848        857        866
TTT CAC TAT ATT CAG AGC AAG CTA GGA ATT GTT TCC CTT CTA CTG GGC ACA ATA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 F   H   Y   I   Q   S   K   L   G   I   V   S   L   L   L   G   T   I

          875        884        893        902        911        920
CAC GCA TTG ATT TTT GCC TGG AAT AAG TGG ATA GAT ATA AAA CAA TTT GTA TGG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 H   A   L   I   F   A   W   N   K   W   I   D   I   K   Q   F   V   W

          929        938        947        956        965        974
TAT ACA CCT CCA ACT TTT ATG ATA GCT GTT TTC CTT CCA ATT GTT GTC CTG ATA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 Y   T   P   P   T   F   M   I   A   V   F   L   P   I   V   V   L   I

          983        992       1001       1010       1019       1028
TTT AAA AGC ATA CTA TTC CTG CCA TGC TTG AGG AAG AAG ATA CTG AAG ATT AGA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 F   K   S   I   L   F   L   P   C   L   R   K   K   I   L   K   I   R

         1037       1046       1055       1064       1073       1082
CAT GGT TGG GAA GAC GTC ACC AAA ATT AAC AAA ACT GAG ATA TGT TCC CAG TTG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 H   G   W   E   D   V   T   K   I   N   K   T   E   I   C   S   Q   L

         1091       1100       1109       1118       1127       1136
TAG AAT TAC TGT TTA CAC ACA TTT TTG TTC AAT ATT GAT ATA TTT TAT CAC CAA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 *   N   Y   C   L   H   T   F   L   F   N   I   D   I   F   Y   H   Q

         1145       1154       1163       1172       1181       1190
CAT TTC AAG TTT GTA TTT GTT AAT AAA ATG ATT ATT CAA GGA AAA AAA AAA AAA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 H   F   K   F   V   F   V   N   K   M   I   I   Q   G   K   K   K   K

AAA AA 3'
--- --
 K
```

FIG. 1C

5' GGC GGA GGC GGA GGC GGA GGG CGA GGG GCG GGG AGC GCC GCC TGG AGC GCG GCA GGT CAT ATT GAA CAT TCC AGA TAC CTA TCA TTA CTC GAT GCT GTT GAT AAC AGC AAG 3' **(SEQ ID NO:3)**

FIG. 4A

GGGGCCCGCACCTCTGGGCAGCAGCGGCAGCCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCC

ATACTATTTTATAGAATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGG

AGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGACCTGTGCTTTTGC

ATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAACTTCAGCACACACAGGAACTCTTTCCACA

GTGGCACTTGCCAATTAAAATAGCTGCTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATT

CACCCCTTAGCAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATGG

TTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAACTTCATAATGGAACCAA

GTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTT

GCTGTACTGCATGCAATTTATAGTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCAT

ATCAACAGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTGTCTCT

GGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCTGTGAGTGACTCTTTGACATGG

AGAGAATTTCACTATATTCAGGTAAATAATATATAAAATAACCCTAAGAGGTAAATCTTCTTTTTGTGTTTATGAT

ATAGAATATGTTGACTTTACCCCATAAAAAATAACAAATGTTTTTCAACAGCAAAGATCTTATACTTGTTCCAATT

AATAATGTGCTCTCCTGTTGTTTTCCCTATTGCTTCTAATTAGGACAAGTGTTTCCTAGACATAAATAAAAGGCAT

TAAAATATTCTTTGTTTTTTTTTTTTGTTTGTTTGTTTTTTGTTTGTTTGTTTGTTTTTTTGAGATGAAGTCTCG

CTCTGTTGCCCATGCTGGAGTACAGTGGCACGATCTCGGCTCACTGCAACCTGCGCCTCCTGGGTTCAGGCGATTC

TCTTGCCTCAGCCTCCTGAGTAGCTGGGATTACAGGCACCCATCACCATGTCCAGCTAATTTTTGTATTTTTAGTA

GAGACAGGGTTTTCCCATGTTGGCCAGGCTGGTCTCGATCTCCTGACCTCAAATGATCCGCCCACCTCGGCCTCCC

AAAGTGCTGGGATGACAGTTGTGAGCCACCACACTCAGCCTGCTCTTTCTAATATTTGAAACTTGTTAGACAATTT

GCTACCCATCTAATGTGATATTTTAGGAATCCAATATGCATGGTTTATTATTTCTTAAAAAAAATATTCTTTTACC

TGTCACCTGAATTTAGTAATGCCTTTTATGTTACACAACTTAGCACTTTCCAGAAACAAAAACTCTCTCCTTGAAA

TAATAGAGTTTTTATCTACCAAAGATATGCTAGTGTCTCATTTCAAAGGCTGCTTTTTCCAGCTTACATTTTATAT

ACTTACTCACTTGAAGTTTCTAAATATTCTTGTAATTTTAAAACTATCTCAGATTTACTGAGGTTTATCTTCTGGT

GGTAGATTATCCATAAGAAGAGTGATGTGCCAGAATCACTCTGGGATCCTTGTCTGACAAGATTCAAAGGACTAAA

TTTAATTCAGTCATGAACACTGCCAATTACCGTTTATGGGTAGACATCTTTGGAAATTTCCACAAGGTCAGACATT

CGCAACTATCCCTTCTACATGTCCACACGTATACTCCAACACTTTATTAGGCATCTGATTAGTTTGGAAAGTATGC

CTCCATCTGAATTAGTCCAGTGTGGCTTAGAGTTGGTACAACATTCTCACAGAATTTCCTAATTTTGTAGGTTCAG

CCTGATAACCACTGGAGTTCTTTGGTCCTCATTAAATAGCTTTCTTCACACATTGCTCTGCCTGTTACACATATGA

TGAACACTGCTTTTTAGACTTCATTAGGAATTTAGGACTGCATCTTGACAACTGAGCCTATTCTACTATATGTACA

FIG. 4B

ATACCTAGCCCATAATAGGTATACAATACACATTTGGTAAAACTAATTTTCAACCAATGACATGTATTTTTCAACT

AGTAACCTAGAAATGTTTCACTTAAAATCTGAGAACTGGTTACACTACAAGTTACCTTGGAGATTCATATATGAAA

ACGCAAACTTAGCTATTTGATTGTATTCACTGGGACTTAAGAATGCGCCTGAATAATTGTGAGTTCGATTTGTTCT

GGCAGGCTAATGACCATTTCCAGTAAAGTGAATAGAGGTCAGAAGTCGTATAAAAGAGGTGTTGTCAGAACACCGT

TGAGATTACATAGGTGAACAACTATTTTTAAGCAACTTTATTTGTGTAGTGACAAAGCATCCCAATGCAGGCTGAA

ATGTTTCATCACATCTCTGGATCTCTCTATTTTGTGCAGACATTGAAAAAATTGTTCATATTATTTCCATGTTATC

AGAATATTTGATTTTTTAAAAACATAGGCCAAGTTCATTCACTTCATTATTCATTTATCAAAATCAGAGTGAATCA

CATTAGTCGCCTTCACAACTGATAAAGATCACTGAAGTCAAATTGATTTTTGCTATAATCTTCAATCTACCTATAT

TTAATTGAGAATCTAAAATGTACAAATCATTGTGTTGATTCTGCAGTGATCCTGCTATAAGTAAGACTCAGTCCCT

GATTTTAGGTATCCTGTGAAAAGCAGAATTAAGACAAATACACAAGAGACAAAGCACAAAAAATAAATATCATAAG

GGGATGAACAAAATGGTGGAGAAAGAGTAGACAAAGTTTTTGATCACCTGCCTTCAAAGAAAGGCTGTGAATTTTG

TTCACTTAGACAGCTTGGAGACAAGAAATTACCCAAAAGTAAGGTGAGGAGGATAGGCAAAAAGAGCAGAAAGATG

TGAATGGACATTGTTGAGAAATGTGATAGGAAAACAATCATAGATAAAGGATTTCCAAGCAACAGAGCATATCCAG

ATGAGGTAGGATGGGATAAACTCTTATTGAACCAATCTTCACCAATTTTGTTTTTCTTTTGCAGAGCAAGCTAGGA

ATTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATAAAACAATTTG

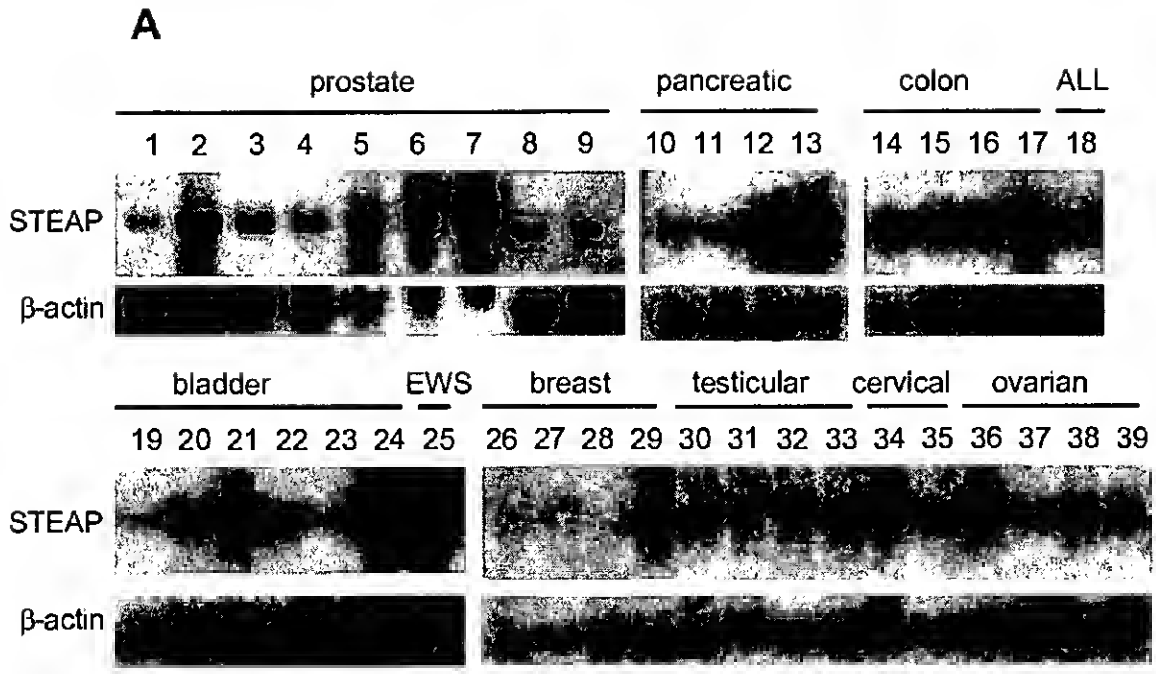
TATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTTGTCCTGATATTTAAAAGCATACTATT

CCTGCCATGCTTGAGGAAGAAGATACTGAAGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAG

ATATGTTCCCAGTTGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATTTCA

AGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAAAA (SEQ ID NO:4)

FIG. 5


A
prostate
pancreatic
colon
ALL
1 2 3 4 5 6 7 8 9
10 11 12 13
14 15 16 17 18
STEAP
β-actin
bladder
EWS
breast
testicular
cervical
ovarian
19 20 21 22 23 24 25
26 27 28 29 30 31 32 33 34 35 36 37 38 39
STEAP
β-actin

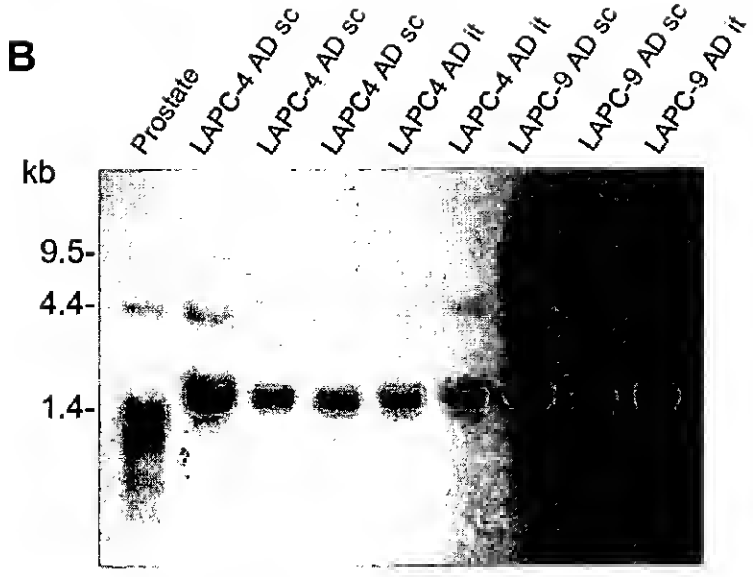

B
Prostate
LAPC-4 AD sc
LAPC-4 AD sc
LAPC4 AD sc
LAPC4 AD it
LAPC-4 AD it
LAPC-9 AD sc
LAPC-9 AD sc
LAPC-9 AD it
kb
9.5-
4.4-
1.4-

FIG. 6

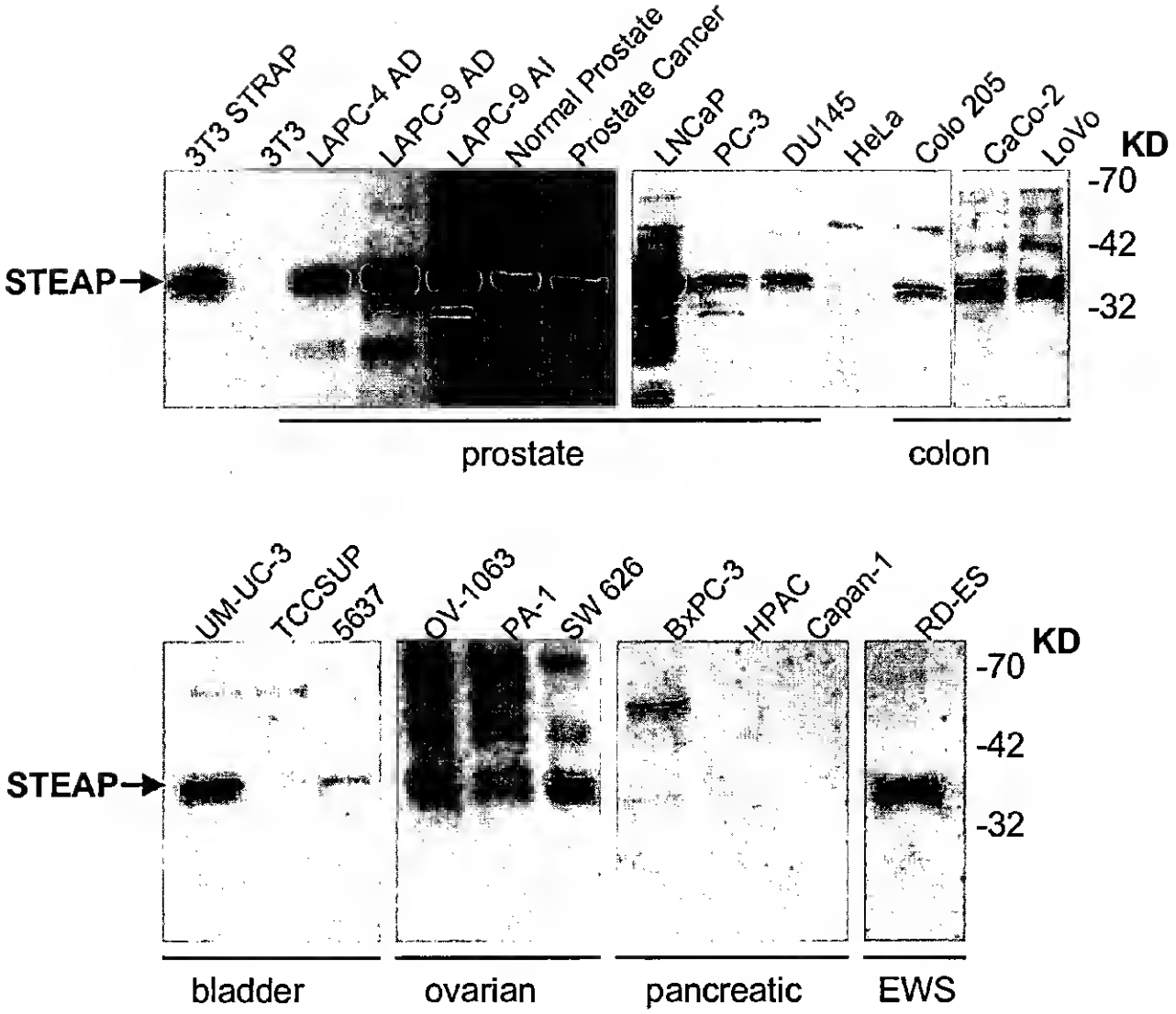

3T3 STRAP
3T3
LAPC-4 AD
LAPC-9 AD
LAPC-9 AI
Normal Prostate
Prostate Cancer
LNCaP
PC-3
DU145
HeLa
Colo 205
CaCo-2
LoVo
KD
-70
-42
-32
STEAP
prostate
colon
UM-UC-3
TCCSUP
5637
OV-1063
PA-1
SW 626
BxPC-3
HPAC
Capan-1
RD-ES
KD
-70
-42
-32
STEAP
bladder
ovarian
pancreatic
EWS

FIG. 7

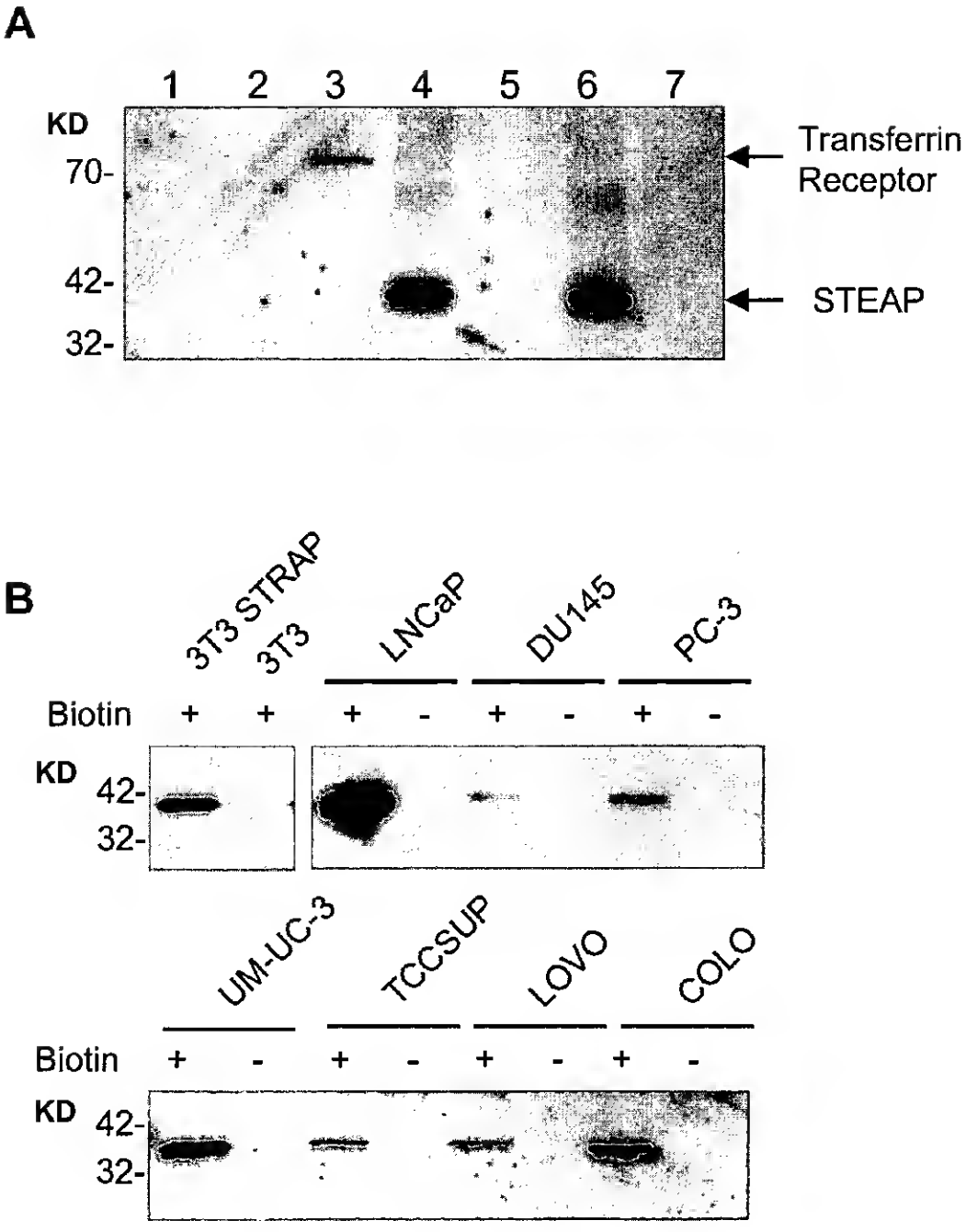
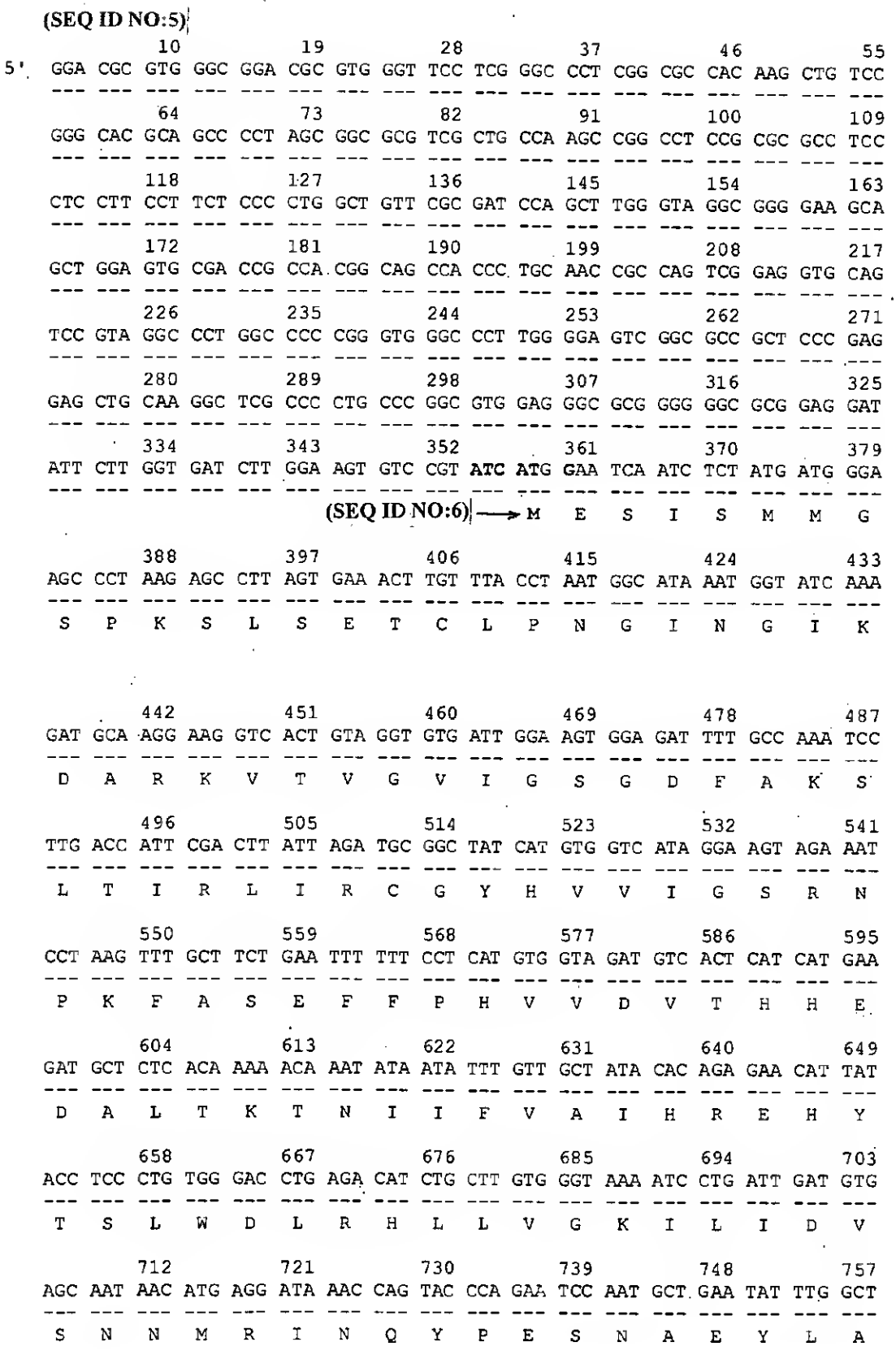

A
1 2 3 4 5 6 7
KD
70-
42-
32-
Transferrin Receptor
STEAP
B
3T3 STRAP
3T3
LNCaP
DU145
PC-3
Biotin + + + - + - + -
KD
42-
32-
UM-UC-3
TCCSUP
LOVO
COLO
Biotin + - + - + - + -
KD
42-
32-

FIG. 9A



```
         766        775        784        793        802        811
TCA TTA TTC CCA GAT TCT TTG ATT GTC AAA GGA TTT AAT GTT GTC TCA GCT TGG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 S   L   F   P   D   S   L   I   V   K   G   F   N   V   V   S   A   W

         820        829        838        847        856        865
GCA CTT CAG TTA GGA CCT AAG GAT GCC AGC CGG CAG GTT TAT ATA TGC AGC AAC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 A   L   Q   L   G   P   K   D   A   S   R   Q   V   Y   I   C   S   N

         874        883        892        901        910        919
AAT ATT CAA GCG CGA CAA CAG GTT ATT GAA CTT GCC CGC CAG TTG AAT TTC ATT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 N   I   Q   A   R   Q   Q   V   I   E   L   A   R   Q   L   N   F   I

         928        937        946        955        964        973
CCC ATT GAC TTG GGA TCC TTA TCA TCA GCC AGA GAG ATT GAA AAT TTA CCC CTA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 P   I   D   L   G   S   L   S   S   A   R   E   I   E   N   L   P   L

         982        991       1000       1009       1018       1027
CGA CTC TTT ACT CTC TGG AGA GGG CCA GTG GTG GTA GCT ATA AGC TTG GCC ACA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 R   L   F   T   L   W   R   G   P   V   V   V   A   I   S   L   A   T

        1036       1045       1054       1063       1072       1081
TTT TTT TTC CTT TAT TCC TTT GTC AGA GAT GTG ATT CAT CCA TAT GCT AGA AAC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 F   F   F   L   Y   S   F   V   R   D   V   I   H   P   Y   A   R   N

-       1090       1099       1108       1117       1126       1135
CAA CAG AGT GAC TTT TAC AAA ATT CCT ATA GAG ATT GTG AAT AAA ACC TTA CCT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 Q   Q   S   D   F   Y   K   I   P   I   E   I   V   N   K   T   L   P

        1144       1153       1162       1171       1180       1189
ATA GTT GCC ATT ACT TTG CTC TCC CTA GTA TAC CTT GCA GGT CTT CTG GCA GCT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 I   V   A   I   T   L   L   S   L   V   Y   L   A   G   L   L   A   A

        1198       1207       1216       1225       1234       1243
GCT TAT CAA CTT TAT TAC GGC ACC AAG TAT AGG AGA TTT CCA CCT TGG TTG GAA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 A   Y   Q   L   Y   Y   G   T   K   Y   R   R   F   P   P   W   L   E

        1252       1261       1270       1279       1288       1297
ACC TGG TTA CAG TGT AGA AAA CAG CTT GGA TTA CTA AGT TTT TTC TTC GCT ATG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 T   W   L   Q   C   R   K   Q   L   G   L   L   S   F   F   F   A   M

        1306       1315       1324       1333       1342       1351
GTC CAT GTT GCC TAC AGC CTC TGC TTA CCG ATG AGA AGG TCA GAG AGA TAT TTG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 V   H   V   A   Y   S   L   C   L   P   M   R   R   S   E   R   Y   L

        1360       1369       1378       1387       1396       1405
TTT CTC AAC ATG GCT TAT CAG CAG GTT CAT GCA AAT ATT GAA AAC TCT TGG AAT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 F   L   N   M   A   Y   Q   Q   V   H   A   N   I   E   N   S   W   N

        1414       1423       1432       1441       1450       1459
GAG GAA GAA GTT TGG AGA ATT GAA ATG TAT ATC TCC TTT GGC ATA ATG AGC CTT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 E   E   E   V   W   R   I   E   M   Y   I   S   F   G   I   M   S   L
```

FIG. 9B

```
      1468        1477        1486        1495        1504        1513
GGC TTA CTT TCC CTC CTG GCA GTC ACT TCT ATC CCT TCA GTG AGC AAT GCT TTA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 G   L   L   S   L   L   A   V   T   S   I   P   S   V   S   N   A   L

      1522        1531        1540        1549        1558        1567
AAC TGG AGA GAA TTC AGT TTT ATT CAG TCT ACA CTT GGA TAT GTC GCT CTG CTC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 N   W   R   E   F   S   F   I   Q   S   T   L   G   Y   V   A   L   L

      1576        1585        1594        1603        1612        1621
ATA AGT ACT TTC CAT GTT TTA ATT TAT GGA TGG AAA CGA GCT TTT GAG GAA GAG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 I   S   T   F   H   V   L   I   Y   G   W   K   R   A   F   E   E   E

      1630        1639        1648        1657        1666        1675
TAC TAC AGA TTT TAT ACA CCA CCA AAC TTT GTT CTT GCT CTT GTT TTG CCC TCA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 Y   Y   R   F   Y   T   P   P   N   F   V   L   A   L   V   L   P   S

      1684        1693        1702        1711        1720        1729
ATT GTA ATT CTG GAT CTT TTG CAG CTT TGC AGA TAC CCA GAC TGA GCT GGA ACT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 I   V   I   L   D   L   L   Q   L   C   R   Y   P   D   *

      1738        1747        1756        1765        1774        1783
GGA ATT TGT CTT CCT ATT GAC TCT ACT TCT TTA AAA GCG GCT GCC CAT TAC ATT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
      1792        1801        1810        1819        1828        1837
CCT CAG CTG TCC TTG CAG TTA GGT GTA CAT GTG ACT GAG TGT TGG CCA GTG AGA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
      1846        1855        1864        1873        1882        1891
TGA AGT CTC CTC AAA GGA AGG CAG CAT GTG TCC TTT TTC ATC CCT TCA TCT TGC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
      1900        1909        1918        1927        1936        1945
TGC TGG GAT TGT GGA TAT AAC AGG AGC CCT GGC AGC TGT CTC CAG AGG ATC AAA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
      1954        1963        1972        1981        1990        1999
GCC ACA CCC AAA GAG TAA GGC AGA TTA GAG ACC AGA AAG ACC TTG ACT ACT TCC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
      2008        2017        2026        2035        2044        2053
CTA CTT CCA CTG CTT TTC CTG CAT TTA AGC CAT TGT AAA TCT GGG TGT GTT ACA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
      2062        2071        2080        2089        2098        2107
TGA AGT GAA AAT TAA TTC TTT CTG CCC TTC AGT TCT TTA TCC TGA TAC CAT TTA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
      2116        2125        2134        2143        2152        2161
ACA CTG TCT GAA TTA ACT AGA CTG CAA TAA TTC TTT CTT TTG AAA GCT TTT AAA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
      2170        2179        2188        2197        2206        2215
GGA TAA TGT GCA ATT CAC ATT AAA ATT GAT TTT CCA TTG TCA ATT AGT TAT ACT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
      2224        2233        2242        2251        2260        2269
CAT TTT CCT GCC TTG ATC TTT CAT TAG ATA TTT TGT ATC TGC TTG GAA TAT ATT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
      2278        2287        2296        2305        2314        2323
ATC TTC TTT TTA ACT GTG TAA TTG GTA ATT ACT AAA ACT CTG TAA TCT CCA AAA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
      2332        2341        2350        2359        2368        2377
TAT TGC TAT CAA ATT ACA CAC CAT GTT TTC TAT CAT TCT CAT AGA TCT GCC TTA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
      2386        2395        2404        2413        2422        2431
TAA ACA TTT AAA TAA AAA GTA CTA TTT AAT GAT TTA AAA AAA AAA AAA AAA AAA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
      2440        2449
AAA AAA AAA AAA AAA AAA AAA AA 3'
--- --- --- --- --- --- --- --
```

FIG. 9C

FIG. 10A-1

(SEQ ID NO:7)

```
   1 CGAAACTTCC CTCTACCCGC CCGGCCCGCG GCGCGCACCG TTGGCGCTGG ACGCTTCCTC
     GCTTTGAAGG GAGATGGGCG GGCCGGGCGC CGCGCGTGGC AACCGCGACC TGCGAAGGAG

                    (SEQ ID NO:8)→M  E  K  T  C  I  D  A  L  P  L  T
  61 CTTGGAAGCG CCTCTCCCTC AGTTATGGAG AAAACTTGTA TAGATGCACT TCCTCTTACT
     GAACCTTCGC GGAGAGGGAG TCAATACCTC TTTTGAACAT ATCTACGTGA AGGAGAATGA

      M  N  S  S  E  K  Q  E  T  V  C  I  F  G  T  G  D  F  G  R
 121 ATGAATTCTT CAGAAAAGCA AGAGACTGTA TGTATTTTTG GAACTGGTGA TTTTGGAAGA
     TACTTAAGAA GTCTTTTCGT TCTCTGACAT ACATAAAAAC CTTGACCACT AAAACCTTCT

      S  L  G  L  K  M  L  Q  C  G  Y  S  V  V  F  G  S  R  N  P
 181 TCACTGGGAT TGAAAATGCT CCAGTGTGGT TATTCTGTTG TTTTTGGAAG TCGAAACCCC
     AGTGACCCTA ACTTTTACGA GGTCACACCA ATAAGACAAC AAAAACCTTC AGCTTTGGGG

      Q  K  T  T  L  L  P  S  G  A  E  V  L  S  Y  S  E  A  A  K
 241 CAGAAGACCA CCCTACTGCC CAGTGGTGCA GAAGTCTTGA GCTATTCAGA AGCAGCCAAG
     GTCTTCTGGT GGGATGACGG GTCACCACGT CTTCAGAACT CGATAAGTCT TCGTCGGTTC

      K  S  G  I  I  I  I  A  I  H  R  E  H  Y  D  F  L  T  E  L
 301 AAGTCTGGCA TCATAATCAT AGCAATCCAC AGAGAGCATT ATGATTTTCT CACAGAATTA
   - TTCAGACCGT AGTATTAGTA TCGTTAGGTG TCTCTCGTAA TACTAAAAGA GTGTCTTAAT

      T  E  V  L  N  G  K  I  L  V  D  I  S  N  N  L  K  I  N  Q
 361 ACTGAGGTTC TCAATGGAAA AATATTGGTA GACATCAGCA ACAACCTCAA AATCAATCAA
     TGACTCCAAG AGTTACCTTT TTATAACCAT CTGTAGTCGT TGTTGGAGTT TTAGTTAGTT

      Y  P  E  S  N  A  E  Y  L  A  H  L  V  P  G  A  H  V  V  K
 421 TATCCAGAAT CTAATGCAGA GTACCTTGCT CATTTGGTGC CAGGAGCCCA CGTGGTAAAA
     ATAGGTCTTA GATTACGTCT CATGGAACGA GTAAACCACG GTCCTCGGGT GCACCATTTT

      A  F  N  T  I  S  A  W  A  L  Q  S  G  A  L  D  A  S  R  Q
 481 GCATTTAACA CCATCTCAGC CTGGGCTCTC CAGTCAGGAG CACTGGATGC AAGTCGGCAG
     CGTAAATTGT GGTAGAGTCG GACCCGAGAG GTCAGTCCTC GTGACCTACG TTCAGCCGTC

      V  F  V  C  G  N  D  S  K  A  K  Q  R  V  M  D  I  V  R  N
 541 GTGTTTGTGT GTGGAAATGA CAGCAAAGCC AAGCAAAGAG TGATGGATAT TGTTCGTAAT
     CACAAACACA CACCTTTACT GTCGTTTCGG TTCGTTTCTC ACTACCTATA ACAAGCATTA

      L  G  L  T  P  M  D  Q  G  S  L  M  A  A  K  E  I  E  K  Y
 601 CTTGGACTTA CTCCAATGGA TCAAGGATCA CTCATGGCAG CCAAAGAAAT TGAAAAGTAC
     GAACCTGAAT GAGGTTACCT AGTTCCTAGT GAGTACCGTC GGTTTCTTTA ACTTTTCATC

      P  L  Q  L  F  P  M  W  R  F  P  F  Y  L  S  A  V  L  C  V
 661 CCCCTGCAGC TATTTCCAAT GTGGAGGTTC CCCTTCTATT TGTCTGCTGT GCTGTGTGTC
     GGGGACGTCG ATAAAGGTTA CACCTCCAAG GGGAAGATAA ACAGACGACA CGACACACAG

      F  L  F  F  Y  C  V  I  R  D  V  I  Y  P  Y  V  Y  E  K  K
 721 TTCTTGTTTT TCTATTGTGT TATAAGAGAC GTAATCTACC CTTATGTTTA TGAAAAGAAA
     AAGAACAAAA AGATAACACA ATATTCTCTG CATTAGATGG GAATACAAAT ACTTTTCTTT
```

```
          D  N  T  F  R  M  A  I  S  I  P  N  R  I  F  P  I  T  A  L
781  GATAATACAT TTCGTATGGC TATTTCCATT CCAAATCGTA TCTTTCCAAT AACAGCACTT
     CTATTATGTA AAGCATACCG ATAAAGGTAA GGTTTAGCAT AGAAAGGTTA TTGTCGTGAA

          T  L  L  A  L  V  Y  L  P  G  V  I  A  A  I  L  Q  L  Y  R
841  ACACTGCTTG CTTTGGTTTA CCTCCCTGGT GTTATTGCTG CCATTCTACA ACTGTACCGA
     TGTGACGAAC GAAACCAAAT GGAGGGACCA CAATAACGAC GGTAAGATGT TGACATGGCT

          G  T  K  Y  R  R  F  P  D  W  L  D  H  W  M  L  C  R  K  Q
901  GGCACAAAAT ACCGTCGATT CCCAGACTGG CTTGACCACT GGATGCTTTG CCGAAAGCAG
     CCGTGTTTTA TGGCAGCTAA GGGTCTGACC GAACTGGTGA CCTACGAAAC GGCTTTCGTC

          L  G  L  V  A  L  G  F  A  F  L  H  V  L  Y  T  L  V  I  P
961  CTTGGCTTGG TAGCTCTGGG ATTTGCCTTC CTTCATGTCC TCTACACACT TGTGATTCCT
     GAACCGAACC ATCGAGACCC TAAACGGAAG GAAGTACAGG AGATGTGTGA ACACTAAGGA

          I  R  Y  Y  V  R  W  R  L  G  N  L  T  V  T  Q  A  I  L  K
1021 ATTCGATATT ATGTACGATG GAGATTGGGA AACTTAACCG TTACCCAGGC AATACTCAAG
     TAAGCTATAA TACATGCTAC CTCTAACCCT TTGAATTGGC AATGGGTCCG TTATGAGTTC

          K  E  N  P  F  S  T  S  S  A  W  L  S  D  S  Y  V  A  L  G
1081 AAGGAGAATC CATTTAGCAC CTCCTCAGCC TGGCTCAGTG ATTCATATGT GGCTTTGGGA
     TTCCTCTTAG GTAAATCGTG GAGGAGTCGG ACCGAGTCAC TAAGTATACA CCGAAACCCT

          I  L  G  F  F  L  F  V  L  L  G  I  T  S  L  P  S  V  S  N
1141 ATACTTGGGT TTTTTCTGTT TGTACTCTTG GGAATCACTT CTTTGCCATC TGTTAGCAAT
     TATGAACCCA AAAAAGACAA ACATGAGAAC CCTTAGTGAA GAAACGGTAG ACAATCGTTA

          A  V  N  W  R  E  F  R  F  V  Q  S  K  L  G  Y  L  T  L  I
1201 GCAGTCAACT GGAGAGAGTT CCGATTTGTC CAGTCCAAAC TGGGTTATTT GACCCTGATC
     CGTCAGTTGA CCTCTCTCAA GGCTAAACAG GTCAGGTTTG ACCCAATAAA CTGGGACTAG

          L  C  T  A  H  T  L  V  Y  G  G  K  R  F  L  S  P  S  N  L
1261 TTGTGTACAG CCCACACCCT GGTGTACGGT GGGAAGAGAT TCCTCAGCCC TTCAAATCTC
     AACACATGTC GGGTGTGGGA CCACATGCCA CCCTTCTCTA AGGAGTCGGG AAGTTTAGAG

          R  W  Y  L  P  A  A  Y  V  L  G  L  I  I  P  C  T  V  L  V
1321 AGATGGTATC TTCCTGCAGC CTACGTGTTA GGGCTTATCA TTCCTTGCAC TGTGCTGGTG
     TCTACCATAG AAGGACGTCG GATGCACAAT CCCGAATAGT AAGGAACGTG ACACGACCAC

          I  K  F  V  L  I  M  P  C  V  D  N  T  L  T  R  I  R  Q  G
1381 ATCAAGTTTG TCCTAATCAT GCCATGTGTA GACAACACCC TTACAAGGAT CCGCCAGGGC
     TAGTTCAAAC AGGATTAGTA CGGTACACAT CTGTTGTGGG AATGTTCCTA GGCGGTCCCG

          W  E  R  N  S  K  H
1441 TGGGAAAGGA ACTCAAAACA CTAGAAAAAG CATTGAATGG AAAATCAATA TTTAAAACAA
     ACCCTTTCCT TGAGTTTTGT GATCTTTTTC GTAACTTACC TTTTAGTTAT AAATTTTGTT

1501 AGTTCAATTT AGCTGGATTT CTGAACTATG GTTTTGAATG TTTAAAGAAG AATGATGGGT
     TCAAGTTAAA TCGACCTAAA GACTTGATAC CAAAACTTAC AAATTTCTTC TTACTACCCA

1561 ACAGTTAGGA AAGTTTTTTT CTTACACCGT GACTGAGGGA AACATTGCTT GTCTTTGAGA
     TGTCAATCCT TTCAAAAAAA GAATGTGGCA CTGACTCCCT TTGTAACGAA CAGAAACTCT

1621 AATTGACTGA CATACTGGAA GAGAACACCA TTTTATCTCA GGTTAGTGAA GAATCAGTGC
     TTAACTGACT GTATGACCTT CTCTTGTGGT AAAATAGAGT CCAATCACTT CTTAGTCACG
```

FIG. 10A-2

```
1681  AGGTCCCTGA C..TTATTTT CCCAGAGGCC ATGGAGCTGA G..TGAGACT AGCCTTGTGG
      TCCAGGGACT GAGAATAAAA GGGTCTCCGG TACCTCGACT CTAACTCTGA TCGGAACACC

1741  TTTCACACTA AAGAGTTTCC TTGTTATGGG CAACATGCAT GACCTAATGT CTTGCAAAAT
      AAAGTGTGAT TTCTCAAAGG AACAATACCC GTTGTACGTA CTGGATTACA GAACGTTTTA

1801  CCAATAGAAG TATTGCAGCT TCCTTCTCTG GCTCAAGGGC TGAGTTAAGT GAAAGGAAAA
      GGTTATCTTC ATAACGTCGA AGGAAGAGAC CGAGTTCCCG ACTCAATTCA CTTTCCTTTT

1861  ACAGCACAAT GGTGACCACT GATAAAGGCT TTATTAGGTA TATCTGAGGA AGTGGGTCAC
      TGTCGTGTTA CCACTGGTGA CTATTTCCGA AATAATCCAT ATAGACTCCT TCACCCAGTG

1921  ATGAAATGTA AAAAGGGAAT GAGGTTTTTG TTGTTTTTTG GAAGTAAAGG CAAACATAAA
      TACTTTACAT TTTTCCCTTA CTCCAAAAAC AACAAAAAAC CTTCATTTCC GTTTGTATTT

1981  TATTACCATG ATGAATTCTA GTGAAATGAC CCCTTGACTT TGCTTTTCTT AATACAGATA
      ATAATGGTAC TACTTAAGAT CACTTTACTG GGGAACTGAA ACGAAAAGAA TTATGTCTAT

2041  TTTACTGAGA GGAACTATTT TTATAACACA AGAAAAATTT ACAATTGATT AAAAGTATCC
      AAATGACTCT CCTTGATAAA AATATTGTGT TCTTTTTAAA TGTTAACTAA TTTTCATAGG

2101  ATGTCTTGGA TACATACGTA TCTATAGAGC TGGCATGTAA TTCTTCCTCT ATAAAGAATA
      TACAGAACCT ATGTATGCAT AGATATCTCG ACCGTACATT AAGAAGGAGA TATTTCTTAT

2161  GGTATAGGAA AGACTGAATA AAAATGGAGG GATATCCCCT TGGATTTCAC TTGCATTGTG
      CCATATCCTT TCTGACTTAT TTTTACCTCC CTATAGGGGA ACCTAAAGTG AACGTAACAC

2221  CAATAAGCAA AGAAGGGTTG ATAAAAGTTC TTGATCAAAA AGTTCAAAGA AACCAGAATT
      GTTATTCGTT TCTTCCCAAC TATTTTCAAG AACTAGTTTT TCAAGTTTCT TTGGTCTTAA

2281  TTAGACAGCA AGCTAAATAA ATATTGTAAA ATTGCACTAT ATTAGGTTAA GTATTATTTA
      AATCTGTCGT TCGATTTATT TATAACATTT TAACGTGATA TAATCCAATT CATAATAAAT

2341  GGTATTATAA TATGCTTTGT AAATTTTATA TTCCAAATAT TGCTCAATAT TTTTCATCTA
      CCATAATATT ATACGAAACA TTTAAAATAT AAGGTTTATA ACGAGTTATA AAAAGTAGAT

2401  TTAAATTAAT TTCTAGTGTA AATAAGTAGC TTCTATATCT GTCTTAGTCT ATTATAATTG
      AATTTAATTA AAGATCACAT TTATTCATCG AAGATATAGA CAGAATCAGA TAATATTAAC

2461  TAAGGAGTAA AATTAAATGA ATAGTCTGCA GGTATAAATT TGAACAATGC ATAGATGATC
      ATTCCTCATT TTAATTTACT TATCAGACGT CCATATTTAA ACTTGTTACG TATCTACTAG

2521  GAAAATTACG GAAAATCATA GGGCAGAGAG GTGTGAAGAT TCATCATTAT GTGAAATTTG
      CTTTTAATGC CTTTTAGTAT CCCGTCTCTC CACACTTCTA AGTAGTAATA CACTTTAAAC

2581  GATCTTTCTC AAATCCTTGC TGAAATTTAG GATGGTTCTC ACTGTTTTTC TGTGCTGATA
      CTAGAAAGAG TTTAGGAACG ACTTTAAATC CTACCAAGAG TGACAAAAAG ACACGACTAT

2641  GTACCCTTTC CAAGGTGACC TTCAGGGGGA TTAACCTTCC TAGCTCAAGC AATGAGCTAA
      CATGGGAAAG GTTCCACTGG AAGTCCCCCT AATTGGAAGG ATCGAGTTCG TTACTCGATT

2701  AAGGAGCCTT ATGCATGATC TTCCCACATA TCAAAATAAC TAAAAGGCAC TGAGTTTGGC
      TTCCTCGGAA TACGTACTAG AAGGGTGTAT AGTTTTATTG ATTTTCCGTG ACTCAAACCG

2761  ATTTTTCTGC CTGCTCTGCT AAGACCTTTT TTTTTTTTTT ACTTTCATTA TAACATATTA
      TAAAAAGACG GACGAGACGA TTCTGGAAAA AAAAAAAAAA TGAAAGTAAT ATTGTATAAT
```

FIG. 10A-3

```
2821  TACATGACAT T. .ACAAAAA TGATTAAAAT ATATTAAAAC A. .ATCAACA ATCCAGGATA
      ATGTACTGTA ATATGTTTTT ACTAATTTTA TATAATTTTG TTGTAGTTGT TAGGTCCTAT

2881  TTTTTCTATA AAACTTTTTA AAAATAATTG TATCTATATA TTCAATTTTA CATCCTTTTT
      AAAAAGATAT TTTGAAAAAT TTTTATTAAC ATAGATATAT AAGTTAAAAT GTAGGAAAAA

2941  CAAAGGCTTT GTTTTTCTAA AGGCTTTGTT TTCCTTTTTA TTATTTTTTT CTTTTTTATT
      GTTTCCGAAA CAAAAAGATT TCCGAAACAA AAGGAAAAAT AATAAAAAAA GAAAAAATAA

3001  TTTTTGAGAC AGTCTTGCTC TGTCGCTCAG GCTGGAGTGC AGTGGCACGA TCTCAGCTCA
      AAAAACTCTG TCAGAACGAG ACAGCGAGTC CGACCTCACG TCACCGTGCT AGAGTCGAGT

3061  CTGCAACCTC CTCCTCCCAG GTTCAAGTGA TTCTTGTTCA TCAGCCTCCC GAGTAGCTGG
      GACGTTGGAG GAGGAGGGTC CAAGTTCACT AAGAACAAGT AGTCGGAGGG CTCATCGACC

3121  GACTACAGGC ATGTGCCACT ATGCCCAGCT AATTTTTGTA CTTTTAGTAG AGACAGGGTT
      CTGATGTCCG TACACGGTGA TACGGGTCGA TTAAAAACAT GAAAATCATC TCTGTCCCAA

3181  TCACCACATT GGTCAGGCTG GTCTTGAAAT GCTGGCGTCA AGTGATCTGC CTGCCTCCGC
      AGTGGTGTAA CCAGTCCGAC CAGAACTTTA CGACCGCAGT TCACTAGACG GACGGAGGCG

3241  CTTACGTAAT ATATTTTCTT AATGGCTGCA TAATATCACA TCAAATAGGC ATTTTTCAAA
      GAATGCATTA TATAAAAGAA TTACCGACGT ATTATAGTGT AGTTTATCCG TAAAAAGTTT

3301  CCTCTTTCCT TATTAAACAT GTAGACTATA TCCATTTTTT ACTAAAATAA ATAACATTTC
      GGAGAAAGGA ATAATTTGTA CATCTGATAT AGGTAAAAAA TGATTTTATT TATTGTAAAG

3361  AGATAATATC TTTGCACTGA TAATGTTGCC AAGCCATTTC TAAAGTGACC TTATCAATTT
      TCTATTATAG AAACGTGACT ATTACAACGG TTCGGTAAAG ATTTCACTGG AATAGTTAAA

3421  AATTACCATT GGATGAGGGT GTTGCTTTCA TCGCACCATT GTAGATTGTC TTTTTTATTT
      TTAATGGTAA CCTACTCCCA CAACGAAAGT AGCGTGGTAA CATCTAACAG AAAAAATAAA

3481  CAATTTGCGT TTATTTATAA CTGGTTGCAA AGGTACACAG AACACACGCT CCTTCAACTT
      GTTAAACGCA AATAAATATT GACCAACGTT TCCATGTGTC TTGTGTGCGA GGAAGTTGAA

3541  ATCTTTGATA AACCCAAGCA AGGATACAAA AAGTTGGACG ACATTGAGTA GAGTCATGGT
      TAGAAACTAT TTGGGTTCGT TCCTATGTTT TTCAACCTGC TGTAACTCAT CTCAGTACCA

3601  ATACGGTGCT GACCCTACAG TATCAGTGGA AAAGATAAGG AAAATGTCAC TACTCACCTA
      TATGCCACGA CTGGGATGTC ATAGTCACCT TTTCTATTCC TTTTACAGTG ATGAGTGGAT

3661  TGTTATGCAA AACAGTTAGG TGTGCTGGGG CTGGATACTG CTCTTTTACT TGAGCATTGG
      ACAATACGTT TTGTCAATCC ACACGACCCC GACCTATGAC GAGAAAATGA ACTCGTAACC

3721  TTGATTAAAG TTTAGGTACC ATCCAGGCTG GTCTAGAGAA GTCTTTGGAG TTAACCATGC
      AACTAATTTC AAATCCATGG TAGGTCCGAC CAGATCTCTT CAGAAACCTC AATTGGTACG

3781  TCTTTTTGTT AAAGAAGAGA GTAATGTGTT TATCCTGGCT CATAGTCCGT CACCGAAAAT
      AGAAAAACAA TTTCTTCTCT CATTACACAA ATAGGACCGA GTATCAGGCA GTGGCTTTTA

3841  AGAAAATGCC ATCCATAGGT AAAATGCTGA CCTATAGAAA AAAATGAACT CTACTTTTAT
      TCTTTTACGG TAGGTATCCA TTTTACGACT GGATATCTTT TTTTACTTGA GATGAAAATA

3901  AGCCTAGTAA AAATGCTCTA CCTGAGTAGT TAAAAGCAAT TCATGAAGCC TGAAGCTAAA
      TCGGATCATT TTTACGAGAT GGACTCATCA ATTTTCGTTA AGTACTTCGG ACTTCGATTT
```

FIG. 10A-4

```
3961  GAGCACTCTG A. GTTTTGG CATAATAGCT GCATTTCCAG A. .GACCTT TGGCCCCAAC
      CTCGTGAGAC TACCAAAACC GTATTATCGA CGTAAAGGTC TGGACTGGAA ACCGGGGTTG

4021  CACAAGTGCT CCAAGCCCCA CCAGCTGACC AAAGAAAGCC CAAGTTCTCC TTCTGTCCTT
      GTGTTCACGA GGTTCGGGGT GGTCGACTGG TTTCTTTCGG GTTCAAGAGG AAGACAGGAA

4081  CCCACAACCT CCCTGCTCCC AAAACTATGA AATTAATTTG ACCATATTAA CACAGCTGAC
      GGGTGTTGGA GGGACGAGGG TTTTGATACT TTAATTAAAC TGGTATAATT GTGTCGACTG

4141  TCCTCCAGTT TACTTAAGGT AGAAAGAATG AGTTTACAAC AGATGAAAAT AAGTGCTTTG
      AGGAGGTCAA ATGAATTCCA TCTTTCTTAC TCAAATGTTG TCTACTTTTA TTCACGAAAC

4201  GGCGAACTGT ATTCCTTTTA ACAGATCCAA ACTATTTTAC ATTTAAAAAA AAAGTTAAAC
      CCGCTTGACA TAAGGAAAAT TGTCTAGGTT TGATAAAATG TAAATTTTTT TTTCAATTTG

4261  TAAACTTCTT TACTGCTGAT ATGTTTCCTG TATTCTAGAA AAATTTTTAC ACTTTCACAT
      ATTTGAAGAA ATGACGACTA TACAAAGGAC ATAAGATCTT TTTAAAAATG TGAAAGTGTA

4321  TATTTTTGTA CACTTTCCCC ATGTTAAGGG ATGATGGCTT TTATAAATGT GTATTCATTA
      ATAAAAACAT GTGAAAGGGG TACAATTCCC TACTACCGAA AATATTTACA CATAAGTAAT

4381  AATGTTACTT TAAAAATAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAA
      TTACAATGAA ATTTTTATTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTT
```

FIG. 10A-5

FIG. 10B

STEAP-2, AA508880 (NCI_CGAP Pr6)
ggtcgacttttccttattcctttgtcagagatctgattcatccatatgctagaaaccaacagagtgacttttaca
aaattcctatagagattgtgaataaaaccttacctatagttgccattactttgctctccctagtataccttgcagg
tcttctggcagctgcttatcaactttattacggcaccaagtataggagatttccaccttggttggaaacctggtta
cagtgtagaaaacagcttggattactaagttgtttcttcgctatggtccatgttgcctacagcctctgcttaccga
tgagaaggtcagagagat **(SEQ ID NO:9)**

STEAP-2, 98P4B6 SSH fragment
TTTGCAGCTTTGCAGATACCCAGACTGAGCTGGAACTGGAATTTGTCTTCCTATTGACTCTACTTCTTTAAAAGCG
GCTGCCCATTACATTCCTCAGCTGTCCTTGCAGTTAGGTGTACATGTGACTGAGTGTTGGCCAGTGAGATGAAGTC
TCCTCAAAGGAAGGCAGCATGTGTCCTTTTT **(SEQ ID NO:10)**

STEAP-3, AI139607 (testis EST)
aagaaggagaatccatttagcacctcctcagcctggctcagtgattcatatgtggctttgggaatacttgggtttt
ttctgtttgtactcttgggaatcacttctttgccatctgttagcaatgcagtcaactggagagagttccgatttgt
ccagtccaaactgggttatttgaccctgatcttgtgtacagcccacaccctggtgtacggtgggaagagattcctc
agcccttcaaatctcagatggtatcttcctgcagcctacgtgttagggcttatcattccttgcactgtgctggtga
tcaagtttgtcctaatcatgccatgtgtagacaacacccttacaaggatccgccagggctgggaaaggaactcaaa
acactagaaaaagcattgaatggaaaatcaatatttaaaacaaagttcaatttagctggaaaaaaaaa
(SEQ ID NO:11)

STEAP 4, R80991 (placental EST)
ggccgcggcanccgctacgacctggtcaacctggcagtcaagcaggtcttggccanacaagagccacctctgggtg
aaggaggaggtctggcggatggagatctacctctccctgggagtgctggccctcggcacgttgtccctgctggccg
tgacctcactgccgtccattgcaaactcgctcaactggagggagttcagcttcgttcagtcctcactgggctttgt
ggccntcgtgctgagcacactncacacgctcacctacggctggacccgcgccttcgaggagagccgctacaagttc
tacctnccteccaccttcacgntcacgctgctggtgccctgcgttcgttcatcctgggccaaagccctgtttntac
tgccttgcattcagccgnaga **(SEQ ID NO:12)**

FIG. 11A-1

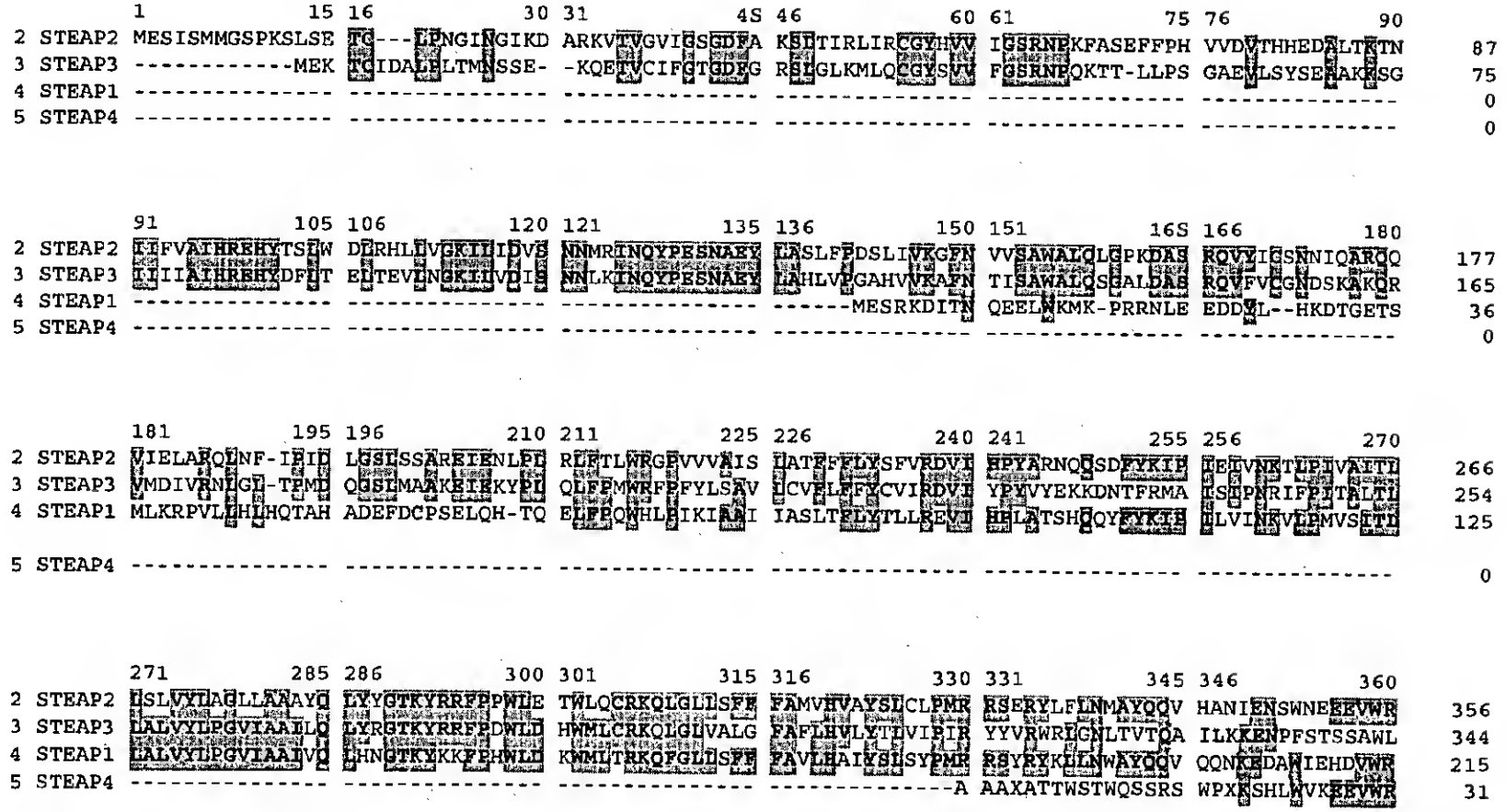


FIG. 11A-2

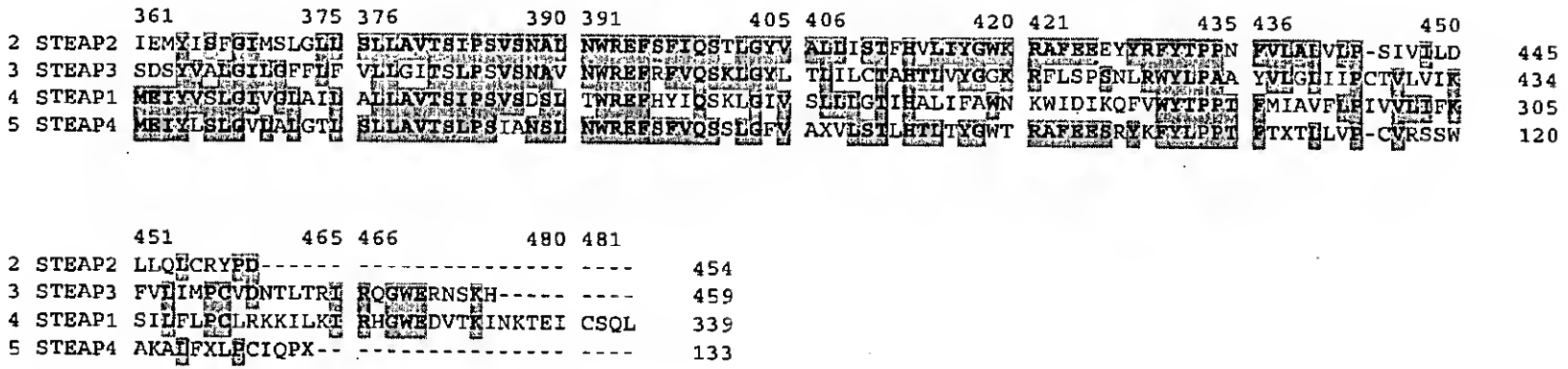

361 375 376 390 391 405 406 420 421 435 436 450
2 STEAP2 IEMYISFGIMSLGLL SLLAVTSIPSVSNAL NWREFSFIQSTLGYV ALLISTFHVLIYGWK RAFEEEYYRFYTPPN FVLAIVLR-SIVLLD 445
3 STEAP3 SDSYVALGILGFFLF VLLGITSLPSVSNAV NWREFRFVQSKLGYL THILCTAHTIVYGGK RFLSPSNLRWYLPAA YVLGLIIPCTVLVIK 434
4 STEAP1 MEIYVSLGIVGLAIL ALLAVTSIPSVSDSL TWREFHYIQSKLGIV SLLLGTIHALIFAWN KWIDIKQFVWYTPPT FMIAVFLPIVVLIFK 305
5 STEAP4 MRIYLSLGVLALGTL SLLAVTSLPSIANSL NWREFSFVQSSLGFV AXVLSTLHTLTYGWT RAFEESRYKFYLPPT FTXTLLVR-CVRSSW 120
451 465 466 480 481
2 STEAP2 LLQLCRYPD------ ---------- ---- 454
3 STEAP3 FVLIMPCVDNTLTRI RQGWERNSKH----- ---- 459
4 STEAP1 SILFLPCLRKKILKT RHGWEDVTKINKTEI CSQL 339
5 STEAP4 AKAIFXLECIQPX-- ---------- ---- 133

FIG. 11B

```
STRAP-1     67 LFPQWHLPIKIAAIIASLTFLYTLLREVIHPLATSHQQYFYKIPILVINKVLPMVSITLL
STRAP-2    208 LFTLWRGPVVVAISLATFFFLYSFVRDVIHPYARNQQSDFYKIPIEIVNKTLPIVAITLL
               ** * * * * *** * **** * * ****** ** ** * ****

STRAP-1    127 ALVYLPGVIAAIVQLHNGTKYKKFPHWLDKWMLTRKQFGLLSFFFAVLHAIYSLSYPMRR
STRAP-2    268 SLVYLAGLLAAAYQLYYGTKYRRFPPWLETWLQCRKQLGLLSFFFAMVHVAYSLCLPMRR
                **** * ** ** **** ** ** * *** ******** * *** ****

STRAP-1    187 SYRYKLLNWAYQQVQQNKEDAWIEHDVWRMEIYVSLGIVGLAILALLAVTSIPSVSDSLT
STRAP-2    328 SERYLFLNMAYQQVHANIENSWNEEEVWRIEMYISFGIMSLGLLSLLAVTSIPSVSNALN
               * ** ** ***** * * * * *** * * * ** * * ********** *

STRAP-1    247 WREFHYIQSKLGIVSLLLGTIHALIFAWNKWIDIKQFVWYTPPTFMIAVFLPIVVLI
STRAP-2    388 WREFSFIQSTLGYVALLISTFHVLIYGWKRAFEEEYYRFYTPPNFVLALVLPSIVIL
               **** *** ** * ** * * ** * **** * * ** *
```

FIG. 11C

```
STEAP1   66 ELFPQWHLPIKIAAIIASLTFLYTLLREVIHPLATSHQQYFYKIPILVINKVLPMVSITL

STEAP3  195 QLFPMWRFPFYLSAVLCVFLFFYCVIRDVIYPYVYEKKDNTFRMAISIPNRIFPITALTL
             *** *  *    *      * *   * ** *             *   *   *    **

STEAP1  126 LALVYLPGVIAAIVQLHNGTKYKKFPHWLDKWMLTRKQFGLLSFFFAVLHAIYSLSYPMR

STEAP3  255 LALVYLPGVIAAILQLYRGTKYRRFPDWLDHWMLCRKQLGLVALGFAFLHVLYTLVIPIR
            ************* **  ****  ** *** *** *** **    ** **  * *  * *

STEAP1  186 RSYRYKLLNWAYQQVQQNKEDAWIEHDVWRMEIYVSLGIVGLAILALLAVTSIPSVSDSL

STEAP3  315 YYVRWRLGNLTVTQAILKKENPFSTSSAWLSDSYVALGILGFFLFVLLGITSLPSVSNAV
              *  * *    *    **       *    ** *** *     **  ** ****

STEAP1  246 TWREFHYIQSKLGIVSLLLGTIHALIFAWNKWIDIKQFVWYTPPTFMIAVFLPIVVLIFK

STEAP3  375 NWREFRFVQSKLGYLTLILCTAHTLVYGGKRFLSPSNLRWYLPAAYVLGLIIPCTVLVIK
             ****   *****   * * * * *              ** *         *  **  *

STEAP1  306 SILFLPCLRKKILKIRHGWEDVTK

STEAP3  435 FVLIMPCVDNTLTRIRQGWERNSK
              *  **       ** ***   *
```

FIG. 11D

```
STEAP2   29 RKVTVGVIGSGDFAKSLTIRLIRCGYHVVIGSRNPKFASEFFPHVVDVTHHEDALTKTNI

STEAP3   18 KQETVCIFGTGDFGRSLGLKMLQCGYSVVFGSRNPQ-KTTLLPSGAEVLSYSEAAKKSGI
               **   * ***  **      *** ** *****       *    *     * *  *

STEAP2   89 IFVAIHREHYTSLWDLRHLLVGKILIDVSNNMRINQYPESNAEYLASLFPDSLIVKGFNV

STEAP3   77 IIIAIHREHYDFLTELTEVLNGKILVDISNNLKINQYPESNAEYLAHLVPGAHVVKAFNT
            *  *******  *  *   * **** * ***. ************* * *    ** **

STEAP2  149 VSAWALQLGPKDASRQVYICSNNIQARQQVIELARQLNFIPIDLGSLSSAREIENLPLRL

STEAP3  137 ISAWALQSGALDASRQVFVCGNDSKAKQRVMDIVRNLGLTPMDQGSLMAAKEIEKYPLQL
             ****** *  ******  * *   * * *    * *   * * ***  * ***  ** *

STEAP2  209 FTLWRGPVVVAISLATFFFLYSFVRDVIHPYARNQQSDFYKIPIEIVNKTLPIVAITLLS

STEAP3  197 FPMWRFPFYLSAVLCVFLFFYCVIRDVIYPYVYEKKDNTFRMAISIPNRIFPITALTLLA
            *  ** *      *  * * *   **** **            * * *   ** * ***

STEAP2  269 LVYLAGLLAAAYQLYYGTKYRRFPPWLETWLQCRKQLGLLSFFFAMVHVAYSLCLPMRRS

STEAP3  257 LVYLPGVIAAILQLYRGTKYRRFPDWLDHWMLCRKQLGLVALGFAFLHVLYTLVIPIRYY
            **** *  **  *** ******** **  *  *******    **  ** * *  * *

STEAP2  329 ERYLFLNMAYQQVHANIENSWNEEEVWRIEMYISFGIMSLGLLSLLAVTSIPSVSNALNW

STEAP3  317 VRWRLGNLTVTQAILKKENPFSTSSAWLSDSYVALGILGFFLFVLLGITSLPSVSNAVNW
             *    *    *    **       *    *   **    *  **  ** ****** **

STEAP2  389 REFSFIQSTLGYVALLISTFHVLIYGWKRAFEEEYYRFYTPPNFVLALVLPSIVIL

STEAP3  377 REFRFVQSKLGYLTLILCTAHTLVYGGKRFLSPSNLRWYLPAAYVLGLIIPCTVLV
            *** * ** ***  *   * * * ** **       * * *   ** *  *  *
```

FIG. 1A-1

(SEQ ID NO:1)

```
                11          20          29          38          47          56
5'  GAG ACT CAC GGT CAA GCT AAG GCG AAG AGT GGG TGG CTG AAG CCA TAC TAT TTT
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---

                65          74          83          92          101         110
    ATA GAA TTA ATG GAA AGC AGA AAA GAC ATC ACA AAC CAA GAA GAA CTT TGG AAA
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
(SEQ ID NO:2)  M   E   S   R   K   D   I   T   N   Q   E   E   L   W   K

                119         128         137         146         155         164
    ATG AAG CCT AGG AGA AAT TTA GAA GAA GAC GAT TAT TTG CAT AAG GAC ACG GGA
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     M   K   P   R   R   N   L   E   E   D   D   Y   L   H   K   D   T   G

                173         182         191         200         209         218
    GAG ACC AGC ATG CTA AAA AGA CCT GTG CTT TTG CAT TTG CAC CAA ACA GCC CAT
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     E   T   S   M   L   K   R   P   V   L   L   H   L   H   Q   T   A   H

                227         236         245         254         263         272
    GCT GAT GAA TTT GAC TGC CCT TCA GAA CTT CAG CAC ACA CAG GAA CTC TTT CCA
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     A   D   E   F   D   C   P   S   E   L   Q   H   T   Q   E   L   F   P

                281         290         299         308         317         326
    CAG TGG CAC TTG CCA ATT AAA ATA GCT GCT ATT ATA GCA TCT CTG ACT TTT CTT
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     Q   W   H   L   P   I   K   I   A   A   I   I   A   S   L   T   F   L

                335         344         353         362         371         380
    TAC ACT CTT CTG AGG GAA GTA ATT CAC CCT TTA GCA ACT TCC CAT CAA CAA TAT
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     Y   T   L   L   R   E   V   I   H   P   L   A   T   S   H   Q   Q   Y

                389         398         407         416         425         434
    TTT TAT AAA ATT CCA ATC CTG GTC ATC AAC AAA GTC TTG CCA ATG GTT TCC ATC
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     F   Y   K   I   P   I   L   V   I   N   K   V   L   P   M   V   S   I

                443         452         461         470         479         488
    ACT CTC TTG GCA TTG GTT TAC CTG CCA GGT GTG ATA GCA GCA ATT GTC CAA CTT
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     T   L   L   A   L   V   Y   L   P   G   V   I   A   A   I   V   Q   L

                497         506         515         524         533         542
    CAT AAT GGA ACC AAG TAT AAG AAG TTT CCA CAT TGG TTG GAT AAG TGG ATG TTA
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     H   N   G   T   K   Y   K   K   F   P   H   W   L   D   K   W   M   L

                551         560         569         578         587         596
    ACA AGA AAG CAG TTT GGG CTT CTC AGT TTC TTT TTT GCT GTA CTG CAT GCA ATT
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     T   R   K   Q   F   G   L   L   S   F   F   F   A   V   L   H   A   I

                605         614         623         632         641         650
    TAT AGT CTG TCT TAC CCA ATG AGG CGA TCC TAC AGA TAC AAG TTG CTA AAC TGG
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     Y   S   L   S   Y   P   M   R   R   S   Y   R   Y   K   L   L   N   W
```

FIG. 1A-2

```
          659        668        677        686        695        704
GCA TAT CAA CAG GTC CAA CAA AAT AAA GAA GAT GCC TGG ATT GAG CAT GAT GTT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 A   Y   Q   Q   V   Q   Q   N   K   E   D   A   W   I   E   H   D   V

          713        722        731        740        749        758
TGG AGA ATG GAG ATT TAT GTG TCT CTG GGA ATT GTG GGA TTG GCA ATA CTG GCT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 W   R   M   E   I   Y   V   S   L   G   I   V   G   L   A   I   L   A

          767        776        785        794        803        812
CTG TTG GCT GTG ACA TCT ATT CCA TCT GTG AGT GAC TCT TTG ACA TGG AGA GAA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 L   L   A   V   T   S   I   P   S   V   S   D   S   L   T   W   R   E

          821        830        839        848        857        866
TTT CAC TAT ATT CAG AGC AAG CTA GGA ATT GTT TCC CTT CTA CTG GGC ACA ATA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 F   H   Y   I   Q   S   K   L   G   I   V   S   L   L   L   G   T   I

          875        884        893        902        911        920
CAC GCA TTG ATT TTT GCC TGG AAT AAG TGG ATA GAT ATA AAA CAA TTT GTA TGG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 H   A   L   I   F   A   W   N   K   W   I   D   I   K   Q   F   V   W

          929        938        947        956        965        974
TAT ACA CCT CCA ACT TTT ATG ATA GCT GTT TTC CTT CCA ATT GTT GTC CTG ATA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 Y   T   P   P   T   F   M   I   A   V   F   L   P   I   V   V   L   I

          983        992       1001       1010       1019       1028
TTT AAA AGC ATA CTA TTC CTG CCA TGC TTG AGG AAG AAG ATA CTG AAG ATT AGA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 F   K   S   I   L   F   L   P   C   L   R   K   K   I   L   K   I   R

         1037       1046       1055       1064       1073       1082
CAT GGT TGG GAA GAC GTC ACC AAA ATT AAC AAA ACT GAG ATA TGT TCC CAG TTG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 H   G   W   E   D   V   T   K   I   N   K   T   E   I   C   S   Q   L

         1091       1100       1109       1118       1127       1136
TAG AAT TAC TGT TTA CAC ACA TTT TTG TTC AAT ATT GAT ATA TTT TAT CAC CAA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 *   N   Y   C   L   H   T   F   L   F   N   I   D   I   F   Y   H   Q

         1145       1154       1163       1172       1181       1190
CAT TTC AAG TTT GTA TTT GTT AAT AAA ATG ATT ATT CAA GGA AAA AAA AAA AAA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 H   F   K   F   V   F   V   N   K   M   I   I   Q   G   K   K   K   K

AAA AA 3'
--- --
 K
```

FIG. 1C

5' GGC GGA GGC GGA GGC GGA GGG CGA GGG GCG GGG AGC GCC GCC TGG AGC GCG

GCA GGT CAT ATT GAA CAT TCC AGA TAC CTA TCA TTA CTC GAT GCT GTT GAT

AAC AGC AAG 3' (SEQ ID NO:3)

FIG. 4A

GGGGCCCGCACCTCTGGGCAGCAGCGGCAGCCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCC

ATACTATTTTATAGAATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGG

AGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGACCTGTGCTTTTGC

ATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAACTTCAGCACACACAGGAACTCTTTCCACA

GTGGCACTTGCCAATTAAAATAGCTGCTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATT

CACCCCTTAGCAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATGG

TTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAACTTCATAATGGAACCAA

GTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTT

GCTGTACTGCATGCAATTTATAGTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCAT

ATCAACAGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTGTCTCT

GGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCTGTGAGTGACTCTTTGACATGG

AGAGAATTTCACTATATTCAGGTAAATAATATATAAAATAACCCTAAGAGGTAAATCTTCTTTTTGTGTTTATGAT

ATAGAATATGTTGACTTTACCCCATAAAAAATAACAAATGTTTTTCAACAGCAAAGATCTTATACTTGTTCCAATT

AATAATGTGCTCTCCTGTTGTTTTCCCTATTGCTTCTAATTAGGACAAGTGTTTCCTAGACATAAATAAAAGGCAT

TAAAATATTCTTTGTTTTTTTTTTTTTGTTTGTTTGTTTTTTGTTTGTTTGTTTGTTTTTTTGAGATGAAGTCTCG

CTCTGTTGCCCATGCTGGAGTACAGTGGCACGATCTCGGCTCACTGCAACCTGCGCCTCCTGGGTTCAGGCGATTC

TCTTGCCTCAGCCTCCTGAGTAGCTGGGATTACAGGCACCCATCACCATGTCCAGCTAATTTTTGTATTTTTAGTA

GAGACAGGGTTTTCCCATGTTGGCCAGGCTGGTCTCGATCTCCTGACCTCAAATGATCCGCCCACCTCGGCCTCCC

AAAGTGCTGGGATGACAGTTGTGAGCCACCACACTCAGCCTGCTCTTTCTAATATTTGAAACTTGTTAGACAATTT

GCTACCCATCTAATGTGATATTTTAGGAATCCAATATGCATGGTTTATTATTTCTTAAAAAAAATATTCTTTTACC

TGTCACCTGAATTTAGTAATGCCTTTTATGTTACACAACTTAGCACTTTCCAGAAACAAAAACTCTCTCCTTGAAA

TAATAGAGTTTTTATCTACCAAAGATATGCTAGTGTCTCATTTCAAAGGCTGCTTTTTCCAGCTTACATTTTATAT

ACTTACTCACTTGAAGTTTCTAAATATTCTTGTAATTTTAAAACTATCTCAGATTTACTGAGGTTTATCTTCTGGT

GGTAGATTATCCATAAGAAGAGTGATGTGCCAGAATCACTCTGGGATCCTTGTCTGACAAGATTCAAAGGACTAAA

TTTAATTCAGTCATGAACACTGCCAATTACCGTTTATGGGTAGACATCTTTGGAAATTTCCACAAGGTCAGACATT

CGCAACTATCCCTTCTACATGTCCACACGTATACTCCAACACTTTATTAGGCATCTGATTAGTTTGGAAAGTATGC

CTCCATCTGAATTAGTCCAGTGTGGCTTAGAGTTGGTACAACATTCTCACAGAATTTCCTAATTTTGTAGGTTCAG

CCTGATAACCACTGGAGTTCTTTGGTCCTCATTAAATAGCTTTCTTCACACATTGCTCTGCCTGTTACACATATGA

TGAACACTGCTTTTTAGACTTCATTAGGAATTTAGGACTGCATCTTGACAACTGAGCCTATTCTACTATATGTACA

FIG. 4B

ATACCTAGCCCATAATAGGTATACAATACACATTTGGTAAAACTAATTTTCAACCAATGACATGTATTTTTCAACT

AGTAACCTAGAAATGTTTCACTTAAAATCTGAGAACTGGTTACACTACAAGTTACCTTGGAGATTCATATATGAAA

ACGCAAACTTAGCTATTTGATTGTATTCACTGGGACTTAAGAATGCGCCTGAATAATTGTGAGTTCGATTTGTTCT

GGCAGGCTAATGACCATTTCCAGTAAAGTGAATAGAGGTCAGAAGTCGTATAAAAGAGGTGTTGTCAGAACACCGT

TGAGATTACATAGGTGAACAACTATTTTTAAGCAACTTTATTTGTGTAGTGACAAAGCATCCCAATGCAGGCTGAA

ATGTTTCATCACATCTCTGGATCTCTCTATTTTGTGCAGACATTGAAAAAATTGTTCATATTATTTCCATGTTATC

AGAATATTTGATTTTTTAAAAACATAGGCCAAGTTCATTCACTTCATTATTCATTTATCAAAATCAGAGTGAATCA

CATTAGTCGCCTTCACAACTGATAAAGATCACTGAAGTCAAATTGATTTTTGCTATAATCTTCAATCTACCTATAT

TTAATTGAGAATCTAAAATGTACAAATCATTGTGTTGATTCTGCAGTGATCCTGCTATAAGTAAGACTCAGTCCCT

GATTTTAGGTATCCTGTGAAAAGCAGAATTAAGACAAATACACAAGAGACAAAGCACAAAAAATAAATATCATAAG

GGGATGAACAAAATGGTGGAGAAAGAGTAGACAAAGTTTTTGATCACCTGCCTTCAAAGAAAGGCTGTGAATTTTG

TTCACTTAGACAGCTTGGAGACAAGAAATTACCCAAAAGTAAGGTGAGGAGGATAGGCAAAAAGAGCAGAAAGATG

TGAATGGACATTGTTGAGAAATGTGATAGGAAAACAATCATAGATAAAGGATTTCCAAGCAACAGAGCATATCCAG

ATGAGGTAGGATGGGATAAACTCTTATTGAACCAATCTTCACCAATTTTGTTTTTCTTTTGCAGAGCAAGCTAGGA

ATTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATAAAACAATTTG

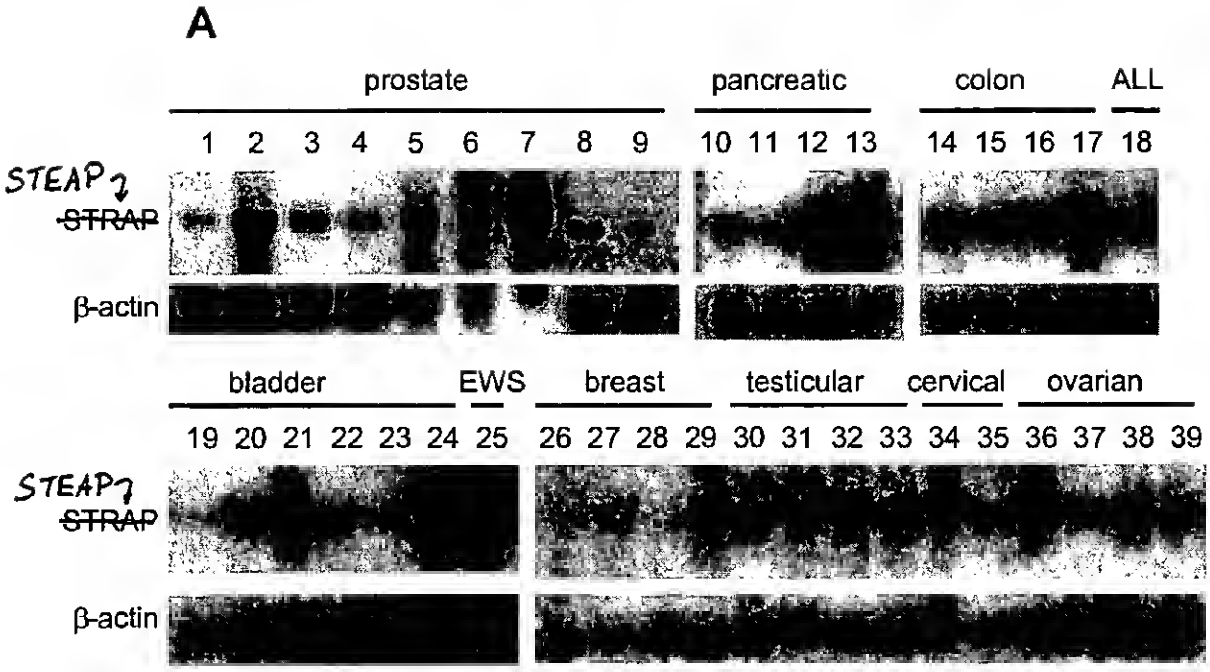
TATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTTGTCCTGATATTTAAAAGCATACTATT

CCTGCCATGCTTGAGGAAGAAGATACTGAAGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAG

ATATGTTCCCAGTTGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATTTCA

AGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAAAA (SEQ ID NO:4)

FIG. 5


A
prostate
pancreatic
colon
ALL
1 2 3 4 5 6 7 8 9
10 11 12 13
14 15 16 17 18
STEAP2
STRAP
β-actin
bladder
EWS
breast
testicular
cervical
ovarian
19 20 21 22 23 24 25
26 27 28 29 30 31 32 33 34 35 36 37 38 39
STEAP2
STRAP
β-actin

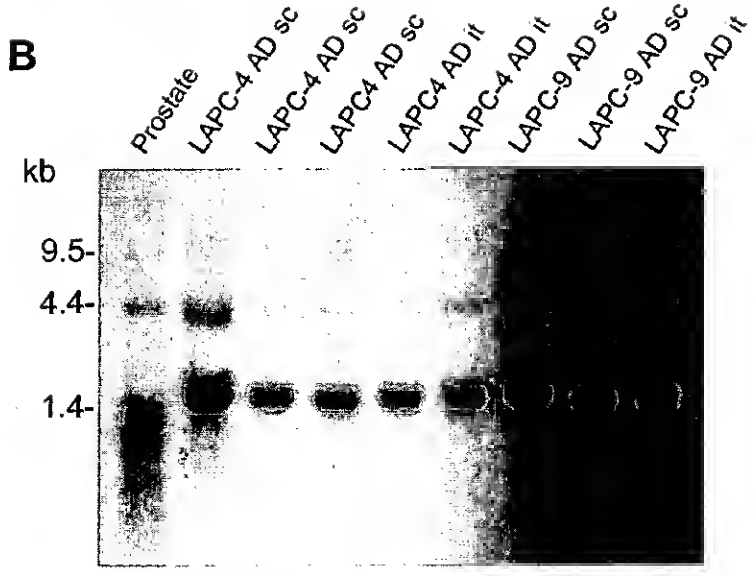

B
Prostate
LAPC-4 AD sc
LAPC-4 AD sc
LAPC4 AD sc
LAPC4 AD it
LAPC-4 AD it
LAPC-9 AD sc
LAPC-9 AD sc
LAPC-9 AD it
kb
9.5-
4.4-
1.4-

FIG. 6

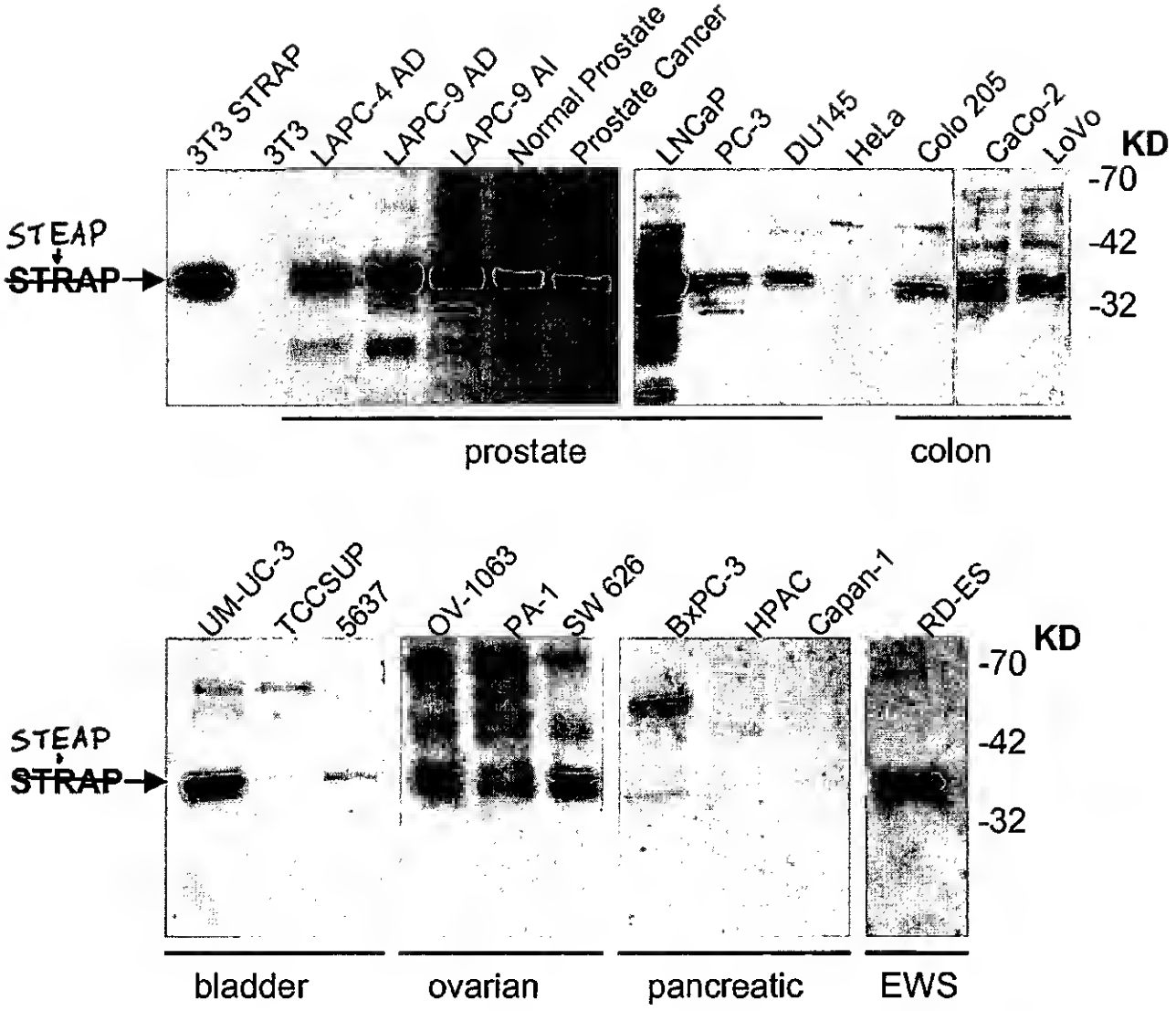

3T3 STRAP
3T3
LAPC-4 AD
LAPC-9 AD
LAPC-9 AI
Normal Prostate
Prostate Cancer
LNCaP
PC-3
DU145
HeLa
Colo 205
CaCo-2
LoVo
KD
-70
-42
-32
STEAP
STRAP
prostate
colon
UM-UC-3
TCCSUP
5637
OV-1063
PA-1
SW 626
BxPC-3
HPAC
Capan-1
RD-ES
KD
-70
-42
-32
STEAP
STRAP
bladder
ovarian
pancreatic
EWS

FIG. 7

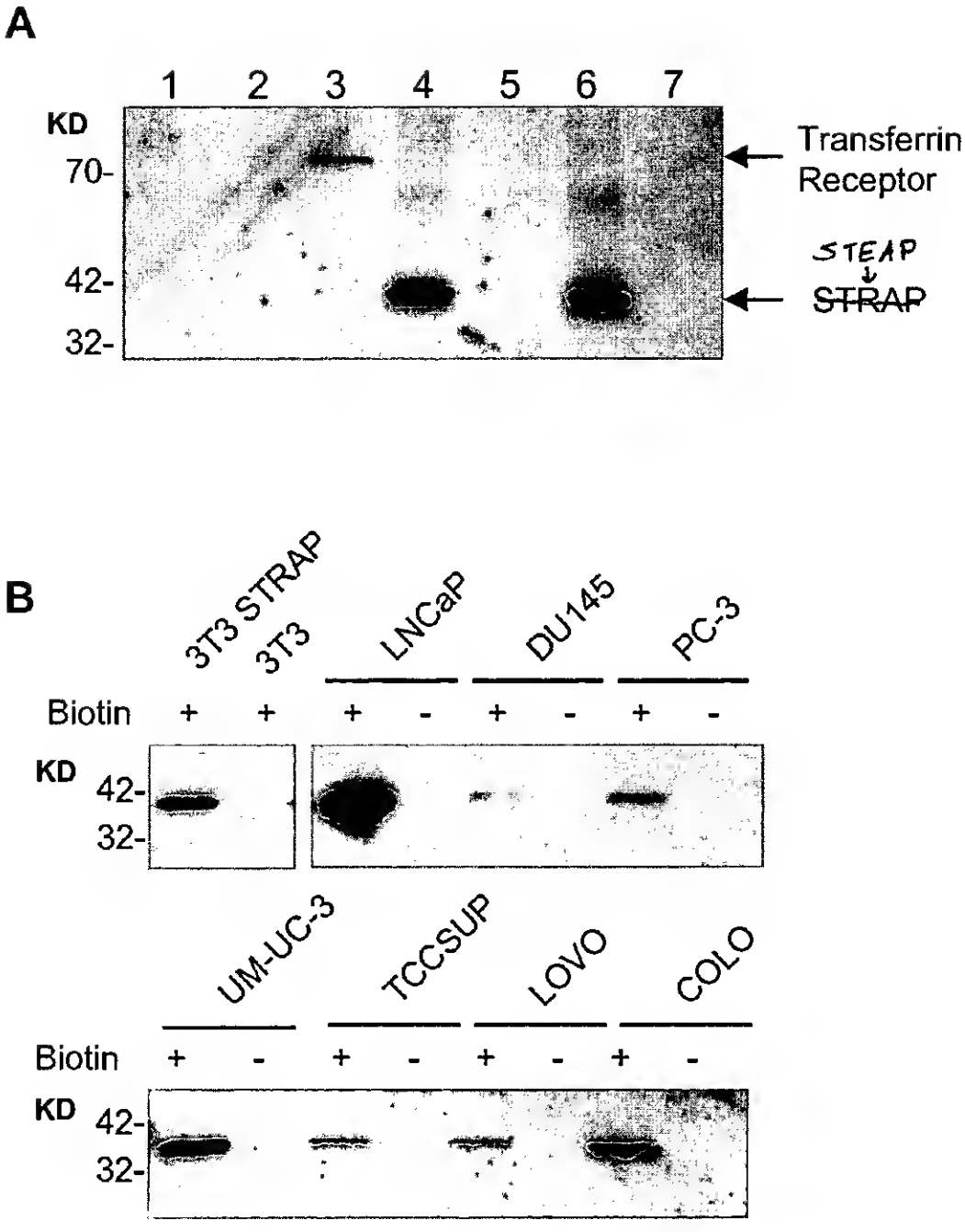

A
1 2 3 4 5 6 7
KD
70-
42-
32-
Transferrin Receptor
STEAP
STRAP
B
3T3 STRAP
3T3
LNCaP
DU145
PC-3
Biotin + + + - + - + -
KD
42-
32-
UM-UC-3
TCCSUP
LOVO
COLO
Biotin + - + - + - + -
KD
42-
32-

FIG. 9A

(SEQ ID NO:5)

```
                10                  19                  28                  37                  46                  55
5'  GGA CGC GTG GGC GGA CGC GTG GGT TCC TCG GGC CCT CGG CGC CAC AAG CTG TCC
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
                64                  73                  82                  91                 100                 109
    GGG CAC GCA GCC CCT AGC GGC GCG TCG CTG CCA AGC CGG CCT CCG CGC GCC TCC
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
               118                 127                 136                 145                 154                 163
    CTC CTT CCT TCT CCC CTG GCT GTT CGC GAT CCA GCT TGG GTA GGC GGG GAA GCA
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
               172                 181                 190                 199                 208                 217
    GCT GGA GTG CGA CCG CCA CGG CAG CCA CCC TGC AAC CGC CAG TCG GAG GTG CAG
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
               226                 235                 244                 253                 262                 271
    TCC GTA GGC CCT GGC CCC CGG GTG GGC CCT TGG GGA GTC GGC GCC GCT CCC GAG
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
               280                 289                 298                 307                 316                 325
    GAG CTG CAA GGC TCG CCC CTG CCC GGC GTG GAG GGC GCG GGG GGC GCG GAG GAT
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
               334                 343                 352                 361                 370                 379
    ATT CTT GGT GAT CTT GGA AGT GTC CGT ATC ATG GAA TCA ATC TCT ATG ATG GGA
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
                                        (SEQ ID NO:6)→M   E   S   I   S   M   M   G

               388                 397                 406                 415                 424                 433
    AGC CCT AAG AGC CTT AGT GAA ACT TGT TTA CCT AAT GGC ATA AAT GGT ATC AAA
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     S   P   K   S   L   S   E   T   C   L   P   N   G   1   N   G   1   K


               442                 451                 460                 469                 478                 487
    GAT GCA AGG AAG GTC ACT GTA GGT GTG ATT GGA AGT GGA GAT TTT GCC AAA TCC
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     D   A   R   K   V   T   V   G   V   I   G   S   G   D   F   A   K   S

               496                 505                 514                 523                 532                 541
    TTG ACC ATT CGA CTT ATT AGA TGC GGC TAT CAT GTG GTC ATA GGA AGT AGA AAT
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     L   T   1   R   L   I   R   C   G   Y   H   V   V   1   G   S   R   N

               550                 559                 568                 577                 586                 595
    CCT AAG TTT GCT TCT GAA TTT TTT CCT CAT GTG GTA GAT GTC ACT CAT CAT GAA
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     P   K   F   A   S   E   F   F   P   H   V   V   D   V   T   H   H   E

               604                 613                 622                 631                 640                 649
    GAT GCT CTC ACA AAA ACA AAT ATA ATA TTT GTT GCT ATA CAC AGA GAA CAT TAT
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     D   A   L   T   K   T   N   1   I   F   V   A   1   H   R   E   H   Y

               658                 667                 676                 685                 694                 703
    ACC TCC CTG TGG GAC CTG AGA CAT CTG CTT GTG GGT AAA ATC CTG ATT GAT GTG
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     T   S   L   W   D   L   R   H   L   L   V   G   K   I   L   I   D   V

               712                 721                 730                 739                 748                 757
    AGC AAT AAC ATG AGG ATA AAC CAG TAC CCA GAA TCC AAT GCT GAA TAT TTG GCT
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     S   N   N   M   R   I   N   Q   Y   P   E   S   N   A   E   Y   L   A
```

```
        766         775         784         793         802         811
TCA TTA TTC CCA GAT TCT TTG ATT GTC AAA GGA TTT AAT GTT GTC TCA GCT TGG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 S   L   F   P   D   S   L   I   V   K   G   F   N   V   V   S   A   W

        820         829         838         847         856         865
GCA CTT CAG TTA GGA CCT AAG GAT GCC AGC CGG CAG GTT TAT ATA TGC AGC AAC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 A   L   Q   L   G   P   K   D   A   S   R   Q   V   Y   I   C   S   N

        874         883         892         901         910         919
AAT ATT CAA GCG CGA CAA CAG GTT ATT GAA CTT GCC CGC CAG TTG AAT TTC ATT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 N   I   Q   A   R   Q   Q   V   I   E   L   A   R   Q   L   N   F   I

        928         937         946         955         964         973
CCC ATT GAC TTG GGA TCC TTA TCA TCA GCC AGA GAG ATT GAA AAT TTA CCC CTA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 P   I   D   L   G   S   L   S   S   A   R   E   I   E   N   L   P   L

        982         991        1000        1009        1018        1027
CGA CTC TTT ACT CTC TGG AGA GGG CCA GTG GTG GTA GCT ATA AGC TTG GCC ACA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 R   L   F   T   L   W   R   G   P   V   V   V   A   I   S   L   A   T

       1036        1045        1054        1063        1072        1081
TTT TTT TTC CTT TAT TCC TTT GTC AGA GAT GTG ATT CAT CCA TAT GCT AGA AAC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 F   F   F   L   Y   S   F   V   R   D   V   I   H   P   Y   A   R   N

-      1090        1099        1108        1117        1126        1135
CAA CAG AGT GAC TTT TAC AAA ATT CCT ATA GAG ATT GTG AAT AAA ACC TTA CCT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 Q   Q   S   D   F   Y   K   I   P   I   E   I   V   N   K   T   L   P

       1144        1153        1162        1171        1180        1189
ATA GTT GCC ATT ACT TTG CTC TCC CTA GTA TAC CTT GCA GGT CTT CTG GCA GCT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 I   V   A   I   T   L   L   S   L   V   Y   L   A   G   L   L   A   A

       1198        1207        1216        1225        1234        1243
GCT TAT CAA CTT TAT TAC GGC ACC AAG TAT AGG AGA TTT CCA CCT TGG TTG GAA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 A   Y   Q   L   Y   Y   G   T   K   Y   R   R   F   P   P   W   L   E

       1252        1261        1270        1279        1288        1297
ACC TGG TTA CAG TGT AGA AAA CAG CTT GGA TTA CTA AGT TTT TTC TTC GCT ATG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 T   W   L   Q   C   R   K   Q   L   G   L   L   S   F   F   F   A   M

       1306        1315        1324        1333        1342        1351
GTC CAT GTT GCC TAC AGC CTC TGC TTA CCG ATG AGA AGG TCA GAG AGA TAT TTG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 V   H   V   A   Y   S   L   C   L   P   M   R   R   S   E   R   Y   L

       1360        1369        1378        1387        1396        1405
TTT CTC AAC ATG GCT TAT CAG CAG GTT CAT GCA AAT ATT GAA AAC TCT TGG AAT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 F   L   N   M   A   Y   Q   Q   V   H   A   N   I   E   N   S   W   N

       1414        1423        1432        1441        1450        1459
GAG GAA GAA GTT TGG AGA ATT GAA ATG TAT ATC TCC TTT GGC ATA ATG AGC CTT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 E   E   E   V   W   R   I   E   M   Y   I   S   F   G   I   M   S   L
```

FIG. 9B

```
      1468       1477       1486       1495       1504       1513
GGC TTA CTT TCC CTC CTG GCA GTC ACT TCT ATC CCT TCA GTG AGC AAT GCT TTA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 G   L   L   S   L   L   A   V   T   S   I   P   S   V   S   N   A   L

      1522       1531       1540       1549       1558       1567
AAC TGG AGA GAA TTC AGT TTT ATT CAG TCT ACA CTT GGA TAT GTC GCT CTG CTC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 N   W   R   E   F   S   F   I   Q   S   T   L   G   Y   V   A   L   L

      1576       1585       1594       1603       1612       1621
ATA AGT ACT TTC CAT GTT TTA ATT TAT GGA TGG AAA CGA GCT TTT GAG GAA GAG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 I   S   T   F   H   V   L   I   Y   G   W   K   R   A   F   E   E   E

      1630       1639       1648       1657       1666       1675
TAC TAC AGA TTT TAT ACA CCA CCA AAC TTT GTT CTT GCT CTT GTT TTG CCC TCA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 Y   Y   R   F   Y   T   P   P   N   F   V   L   A   L   V   L   P   S

      1684       1693       1702       1711       1720       1729
ATT GTA ATT CTG GAT CTT TTG CAG CTT TGC AGA TAC CCA GAC TGA GCT GGA ACT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 I   V   I   L   D   L   L   Q   L   C   R   Y   P   D   *

      1738       1747       1756       1765       1774       1783
GGA ATT TGT CTT CCT ATT GAC TCT ACT TCT TTA AAA GCG GCT GCC CAT TAC ATT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
      1792       1801       1810       1819       1828       1837
CCT CAG CTG TCC TTG CAG TTA GGT GTA CAT GTG ACT GAG TGT TGG CCA GTG AGA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
      1846       1855       1864       1873       1882       1891
TGA AGT CTC CTC AAA GGA AGG CAG CAT GTG TCC TTT TTC ATC CCT TCA TCT TGC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
      1900       1909       1918       1927       1936       1945
TGC TGG GAT TGT GGA TAT AAC AGG AGC CCT GGC AGC TGT CTC CAG AGG ATC AAA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
      1954       1963       1972       1981       1990       1999
GCC ACA CCC AAA GAG TAA GGC AGA TTA GAG ACC AGA AAG ACC TTG ACT ACT TCC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
      2008       2017       2026       2035       2044       2053
CTA CTT CCA CTG CTT TTC CTG CAT TTA AGC CAT TGT AAA TCT GGG TGT GTT ACA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
      2062       2071       2080       2089       2098       2107
TGA AGT GAA AAT TAA TTC TTT CTG CCC TTC AGT TCT TTA TCC TGA TAC CAT TTA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
      2116       2125       2134       2143       2152       2161
ACA CTG TCT GAA TTA ACT AGA CTG CAA TAA TTC TTT CTT TTG AAA GCT TTT AAA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
      2170       2179       2188       2197       2206       2215
GGA TAA TGT GCA ATT CAC ATT AAA ATT GAT TTT CCA TTG TCA ATT AGT TAT ACT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
      2224       2233       2242       2251       2260       2269
CAT TTT CCT GCC TTG ATC TTT CAT TAG ATA TTT TGT ATC TGC TTG GAA TAT ATT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
      2278       2287       2296       2305       2314       2323
ATC TTC TTT TTA ACT GTG TAA TTG GTA ATT ACT AAA ACT CTG TAA TCT CCA AAA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
      2332       2341       2350       2359       2368       2377
TAT TGC TAT CAA ATT ACA CAC CAT GTT TTC TAT CAT TCT CAT AGA TCT GCC TTA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
      2386       2395       2404       2413       2422       2431
TAA ACA TTT AAA TAA AAA GTA CTA TTT AAT GAT TTA AAA AAA AAA AAA AAA AAA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
      2440       2449
AAA AAA AAA AAA AAA AAA AAA AA 3'
--- --- --- --- --- --- --- --
```

FIG. 9C

FIG. 10A-1

(SEQ ID NO:7)

```
1   CGAAACTTCC CTCTACCCGC CCGGCCCGCG GCGCGCACCG TTGGCGCTGG ACGCTTCCTC
    GCTTTGAAGG GAGATGGGCG GGCCGGGCGC CGCGCGTGGC AACCGCGACC TGCGAAGGAG

                (SEQ ID NO:8)→M  E  K  T  C  I  D  A  L  P  L  T
61  CTTGGAAGCG CCTCTCCCTC AGTTATGGAG AAAACTTGTA TAGATGCACT TCCTCTTACT
    GAACCTTCGC GGAGAGGGAG TCAATACCTC TTTTGAACAT ATCTACGTGA AGGAGAATGA

     M  N  S  S  E  K  Q  E  T  V  C  I  F  G  T  G  D  F  G  R
121 ATGAATTCTT CAGAAAAGCA AGAGACTGTA TGTATTTTTG GAACTGGTGA TTTTGGAAGA
    TACTTAAGAA GTCTTTTCGT TCTCTGACAT ACATAAAAAC CTTGACCACT AAAACCTTCT

     S  L  G  L  K  M  L  Q  C  G  Y  S  V  V  F  G  S  R  N  P
181 TCACTGGGAT TGAAAATGCT CCAGTGTGGT TATTCTGTTG TTTTTGGAAG TCGAAACCCC
    AGTGACCCTA ACTTTTACGA GGTCACACCA ATAAGACAAC AAAAACCTTC AGCTTTGGGG

     Q  K  T  T  L  L  P  S  G  A  E  V  L  S  Y  S  E  A  A  K
241 CAGAAGACCA CCCTACTGCC CAGTGGTGCA GAAGTCTTGA GCTATTCAGA AGCAGCCAAG
    GTCTTCTGGT GGGATGACGG GTCACCACGT CTTCAGAACT CGATAAGTCT TCGTCGGTTC

     K  S  G  I  I  I  I  A  I  H  R  E  H  Y  D  F  L  T  E  L
301 AAGTCTGGCA TCATAATCAT AGCAATCCAC AGAGAGCATT ATGATTTTCT CACAGAATTA
  - TTCAGACCGT AGTATTAGTA TCGTTAGGTG TCTCTCGTAA TACTAAAAGA GTGTCTTAAT

     T  E  V  L  N  G  K  I  L  V  D  I  S  N  N  L  K  I  N  Q
361 ACTGAGGTTC TCAATGGAAA AATATTGGTA GACATCAGCA ACAACCTCAA AATCAATCAA
    TGACTCCAAG AGTTACCTTT TTATAACCAT CTGTAGTCGT TGTTGGAGTT TTAGTTAGTT

     Y  P  E  S  N  A  E  Y  L  A  H  L  V  P  G  A  H  V  V  K
421 TATCCAGAAT CTAATGCAGA GTACCTTGCT CATTTGGTGC CAGGAGCCCA CGTGGTAAAA
    ATAGGTCTTA GATTACGTCT CATGGAACGA GTAAACCACG GTCCTCGGGT GCACCATTTT

     A  F  N  T  I  S  A  W  A  L  Q  S  G  A  L  D  A  S  R  Q
481 GCATTTAACA CCATCTCAGC CTGGGCTCTC CAGTCAGGAG CACTGGATGC AAGTCGGCAG
    CGTAAATTGT GGTAGAGTCG GACCCGAGAG GTCAGTCCTC GTGACCTACG TTCAGCCGTC

     V  F  V  C  G  N  D  S  K  A  K  Q  R  V  M  D  I  V  R  N
541 GTGTTTGTGT GTGGAAATGA CAGCAAAGCC AAGCAAAGAG TGATGGATAT TGTTCGTAAT
    CACAAACACA CACCTTTACT GTCGTTTCGG TTCGTTTCTC ACTACCTATA ACAAGCATTA

     L  G  L  T  P  M  D  Q  G  S  L  M  A  A  K  E  I  E  K  Y
601 CTTGGACTTA CTCCAATGGA TCAAGGATCA CTCATGGCAG CCAAAGAAAT TGAAAAGTAC
    GAACCTGAAT GAGGTTACCT AGTTCCTAGT GAGTACCGTC GGTTTCTTTA ACTTTTCATG

     P  L  Q  L  F  P  M  W  R  F  P  F  Y  L  S  A  V  L  C  V
661 CCCCTGCAGC TATTTCCAAT GTGGAGGTTC CCCTTCTATT TGTCTGCTGT GCTGTGTGTC
    GGGGACGTCG ATAAAGGTTA CACCTCCAAG GGGAAGATAA ACAGACGACA CGACACACAG

     F  L  F  F  Y  C  V  I  R  D  V  I  Y  P  Y  V  Y  E  K  K
721 TTCTTGTTTT TCTATTGTGT TATAAGAGAC GTAATCTACC CTTATGTTTA TGAAAAGAAA
    AAGAACAAAA AGATAACACA ATATTCTCTG CATTAGATGG GAATACAAAT ACTTTTCTTT
```

```
          D  N  T  F  R  M  A  I  S  I  P  N  R  I  F  P  I  T  A  L
781  GATAATACAT TTCGTATGGC TATTTCCATT CCAAATCGTA TCTTTCCAAT AACAGCACTT
     CTATTATGTA AAGCATACCG ATAAAGGTAA GGTTTAGCAT AGAAAGGTTA TTGTCGTGAA

          T  L  L  A  L  V  Y  L  P  G  V  I  A  A  I  L  Q  L  Y  R
841  ACACTGCTTG CTTTGGTTTA CCTCCCTGGT GTTATTGCTG CCATTCTACA ACTGTACCGA
     TGTGACGAAC GAAACCAAAT GGAGGGACCA CAATAACGAC GGTAAGATGT TGACATGGCT

          G  T  K  Y  R  R  F  P  D  W  L  D  H  W  M  L  C  R  K  Q
901  GGCACAAAAT ACCGTCGATT CCCAGACTGG CTTGACCACT GGATGCTTTG CCGAAAGCAG
     CCGTGTTTTA TGGCAGCTAA GGGTCTGACC GAACTGGTGA CCTACGAAAC GGCTTTCGTC

          L  G  L  V  A  L  G  F  A  F  L  H  V  L  Y  T  L  V  I  P
961  CTTGGCTTGG TAGCTCTGGG ATTTGCCTTC CTTCATGTCC TCTACACACT TGTGATTCCT
     GAACCGAACC ATCGAGACCC TAAACGGAAG GAAGTACAGG AGATGTGTGA ACACTAAGGA

          I  R  Y  Y  V  R  W  R  L  G  N  L  T  V  T  Q  A  I  L  K
1021 ATTCGATATT ATGTACGATG GAGATTGGGA AACTTAACCG TTACCCAGGC AATACTCAAG
     TAAGCTATAA TACATGCTAC CTCTAACCCT TTGAATTGGC AATGGGTCCG TTATGAGTTC

          K  E  N  P  F  S  T  S  S  A  W  L  S  D  S  Y  V  A  L  G
1081 AAGGAGAATC CATTTAGCAC CTCCTCAGCC TGGCTCAGTG ATTCATATGT GGCTTTGGGA
     TTCCTCTTAG GTAAATCGTG GAGGAGTCGG ACCGAGTCAC TAAGTATACA CCGAAACCCT

          I  L  G  F  F  L  F  V  L  L  G  I  T  S  L  P  S  V  S  N
1141 ATACTTGGGT TTTTTCTGTT TGTACTCTTG GGAATCACTT CTTTGCCATC TGTTAGCAAT
     TATGAACCCA AAAAAGACAA ACATGAGAAC CCTTAGTGAA GAAACGGTAG ACAATCGTTA

          A  V  N  W  R  E  F  R  F  V  Q  S  K  L  G  Y  L  T  L  I
1201 GCAGTCAACT GGAGAGAGTT CCGATTTGTC CAGTCCAAAC TGGGTTATTT GACCCTGATC
     CGTCAGTTGA CCTCTCTCAA GGCTAAACAG GTCAGGTTTG ACCCAATAAA CTGGGACTAG

          L  C  T  A  H  T  L  V  Y  G  G  K  R  F  L  S  P  S  N  L
1261 TTGTGTACAG CCCACACCCT GGTGTACGGT GGGAAGAGAT TCCTCAGCCC TTCAAATCTC
     AACACATGTC GGGTGTGGGA CCACATGCCA CCCTTCTCTA AGGAGTCGGG AAGTTTAGAG

          R  W  Y  L  P  A  A  Y  V  L  G  L  I  I  P  C  T  V  L  V
1321 AGATGGTATC TTCCTGCAGC CTACGTGTTA GGGCTTATCA TTCCTTGCAC TGTGCTGGTG
     TCTACCATAG AAGGACGTCG GATGCACAAT CCCGAATAGT AAGGAACGTG ACACGACCAC

          I  K  F  V  L  I  M  P  C  V  D  N  T  L  T  R  I  R  Q  G
1381 ATCAAGTTTG TCCTAATCAT GCCATGTGTA GACAACACCC TTACAAGGAT CCGCCAGGGC
     TAGTTCAAAC AGGATTAGTA CGGTACACAT CTGTTGTGGG AATGTTCCTA GGCGGTCCCG

          W  E  R  N  S  K  H
1441 TGGGAAAGGA ACTCAAAACA CTAGAAAAAG CATTGAATGG AAAATCAATA TTTAAAACAA
     ACCCTTTCCT TGAGTTTTGT GATCTTTTTC GTAACTTACC TTTTAGTTAT AAATTTTGTT

1501 AGTTCAATTT AGCTGGATTT CTGAACTATG GTTTTGAATG TTTAAAGAAG AATGATGGGT
     TCAAGTTAAA TCGACCTAAA GACTTGATAC CAAAACTTAC AAATTTCTTC TTACTACCCA

1561 ACAGTTAGGA AAGTTTTTTT CTTACACCGT GACTGAGGGA AACATTGCTT GTCTTTGAGA
     TGTCAATCCT TTCAAAAAAA GAATGTGGCA CTGACTCCCT TTGTAACGAA CAGAAACTCT

1621 AATTGACTGA CATACTGGAA GAGAACACCA TTTTATCTCA GGTTAGTGAA GAATCAGTGC
     TTAACTGACT GTATGACCTT CTCTTGTGGT AAAATAGAGT CCAATCACTT CTTAGTCACG
```

FIG. 10A-2

```
1681  AGGTCCCTGA C..fTATTTT CCCAGAGGCC ATGGAGCTGA G..fGAGACT AGCCTTGTGG
      TCCAGGGACT GAGAATAAAA GGGTCTCCGG TACCTCGACT CTAACTCTGA TCGGAACACC

1741  TTTCACACTA AAGAGTTTCC TTGTTATGGG CAACATGCAT GACCTAATGT CTTGCAAAAT
      AAAGTGTGAT TTCTCAAAGG AACAATACCC GTTGTACGTA CTGGATTACA GAACGTTTTA

1801  CCAATAGAAG TATTGCAGCT TCCTTCTCTG GCTCAAGGGC TGAGTTAAGT GAAAGGAAAA
      GGTTATCTTC ATAACGTCGA AGGAAGAGAC CGAGTTCCCG ACTCAATTCA CTTTCCTTTT

1861  ACAGCACAAT GGTGACCACT GATAAAGGCT TTATTAGGTA TATCTGAGGA AGTGGGTCAC
      TGTCGTGTTA CCACTGGTGA CTATTTCCGA AATAATCCAT ATAGACTCCT TCACCCAGTG

1921  ATGAAATGTA AAAAGGGAAT GAGGTTTTTG TTGTTTTTTG GAAGTAAAGG CAAACATAAA
      TACTTTACAT TTTTCCCTTA CTCCAAAAAC AACAAAAAAC CTTCATTTCC GTTTGTATTT

1981  TATTACCATG ATGAATTCTA GTGAAATGAC CCCTTGACTT TGCTTTTCTT AATACAGATA
      ATAATGGTAC TACTTAAGAT CACTTTACTG GGGAACTGAA ACGAAAAGAA TTATGTCTAT

2041  TTTACTGAGA GGAACTATTT TTATAACACA AGAAAAATTT ACAATTGATT AAAAGTATCC
      AAATGACTCT CCTTGATAAA AATATTGTGT TCTTTTTAAA TGTTAACTAA TTTTCATAGG

2101  ATGTCTTGGA TACATACGTA TCTATAGAGC TGGCATGTAA TTCTTCCTCT ATAAAGAATA
      TACAGAACCT ATGTATGCAT AGATATCTCG ACCGTACATT AAGAAGGAGA TATTTCTTAT

2161  GGTATAGGAA AGACTGAATA AAAATGGAGG GATATCCCCT TGGATTTCAC TTGCATTGTG
      CCATATCCTT TCTGACTTAT TTTTACCTCC CTATAGGGGA ACCTAAAGTG AACGTAACAC

2221  CAATAAGCAA AGAAGGGTTG ATAAAAGTTC TTGATCAAAA AGTTCAAAGA AACCAGAATT
      GTTATTCGTT TCTTCCCAAC TATTTTCAAG AACTAGTTTT TCAAGTTTCT TTGGTCTTAA

2281  TTAGACAGCA AGCTAAATAA ATATTGTAAA ATTGCACTAT ATTAGGTTAA GTATTATTTA
      AATCTGTCGT TCGATTTATT TATAACATTT TAACGTGATA TAATCCAATT CATAATAAAT

2341  GGTATTATAA TATGCTTTGT AAATTTTATA TTCCAAATAT TGCTCAATAT TTTTCATCTA
      CCATAATATT ATACGAAACA TTTAAAATAT AAGGTTTATA ACGAGTTATA AAAAGTAGAT

2401  TTAAATTAAT TTCTAGTGTA AATAAGTAGC TTCTATATCT GTCTTAGTCT ATTATAATTG
      AATTTAATTA AAGATCACAT TTATTCATCG AAGATATAGA CAGAATCAGA TAATATTAAC

2461  TAAGGAGTAA AATTAAATGA ATAGTCTGCA GGTATAAATT TGAACAATGC ATAGATGATC
      ATTCCTCATT TTAATTTACT TATCAGACGT CCATATTTAA ACTTGTTACG TATCTACTAG

2521  GAAAATTACG GAAAATCATA GGGCAGAGAG GTGTGAAGAT TCATCATTAT GTGAAATTTG
      CTTTTAATGC CTTTTAGTAT CCCGTCTCTC CACACTTCTA AGTAGTAATA CACTTTAAAC

2581  GATCTTTCTC AAATCCTTGC TGAAATTTAG GATGGTTCTC ACTGTTTTTC TGTGCTGATA
      CTAGAAAGAG TTTAGGAACG ACTTTAAATC CTACCAAGAG TGACAAAAAG ACACGACTAT

2641  GTACCCTTTC CAAGGTGACC TTCAGGGGGA TTAACCTTCC TAGCTCAAGC AATGAGCTAA
      CATGGGAAAG GTTCCACTGG AAGTCCCCCT AATTGGAAGG ATCGAGTTCG TTACTCGATT

2701  AAGGAGCCTT ATGCATGATC TTCCCACATA TCAAAATAAC TAAAAGGCAC TGAGTTTGGC
      TTCCTCGGAA TACGTACTAG AAGGGTGTAT AGTTTTATTG ATTTTCCGTG ACTCAAACCG

2761  ATTTTTCTGC CTGCTCTGCT AAGACCTTTT TTTTTTTTTT ACTTTCATTA TAACATATTA
      TAAAAAGACG GACGAGACGA TTCTGGAAAA AAAAAAAAAA TGAAAGTAAT ATTGTATAAT
```

FIG. 10A-3

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2821  TACATGACAT T. .ACAAAAA TGATTAAAAT ATATTAAAAC A. .ATCAACA ATCCAGGATA
      ATGTACTGTA ATATGTTTTT ACTAATTTTA TATAATTTTG TTGTAGTTGT TAGGTCCTAT

2881  TTTTTCTATA AAACTTTTTA AAAATAATTG TATCTATATA TTCAATTTTA CATCCTTTTT
      AAAAAGATAT TTTGAAAAAT TTTTATTAAC ATAGATATAT AAGTTAAAAT GTAGGAAAAA

2941  CAAAGGCTTT GTTTTTCTAA AGGCTTTGTT TTCCTTTTTA TTATTTTTTT CTTTTTTATT
      GTTTCCGAAA CAAAAAGATT TCCGAAACAA AAGGAAAAAT AATAAAAAAA GAAAAAATAA

3001  TTTTTGAGAC AGTCTTGCTC TGTCGCTCAG GCTGGAGTGC AGTGGCACGA TCTCAGCTCA
      AAAAACTCTG TCAGAACGAG ACAGCGAGTC CGACCTCACG TCACCGTGCT AGAGTCGAGT

3061  CTGCAACCTC CTCCTCCCAG GTTCAAGTGA TTCTTGTTCA TCAGCCTCCC GAGTAGCTGG
      GACGTTGGAG GAGGAGGGTC CAAGTTCACT AAGAACAAGT AGTCGGAGGG CTCATCGACC

3121  GACTACAGGC ATGTGCCACT ATGCCCAGCT AATTTTTGTA CTTTTAGTAG AGACAGGGTT
      CTGATGTCCG TACACGGTGA TACGGGTCGA TTAAAAACAT GAAAATCATC TCTGTCCCAA

3181  TCACCACATT GGTCAGGCTG GTCTTGAAAT GCTGGCGTCA AGTGATCTGC CTGCCTCCGC
      AGTGGTGTAA CCAGTCCGAC CAGAACTTTA CGACCGCAGT TCACTAGACG GACGGAGGCG

3241  CTTACGTAAT ATATTTTCTT AATGGCTGCA TAATATCACA TCAAATAGGC ATTTTTCAAA
      GAATGCATTA TATAAAAGAA TTACCGACGT ATTATAGTGT AGTTTATCCG TAAAAAGTTT

3301  CCTCTTTCCT TATTAAACAT GTAGACTATA TCCATTTTTT ACTAAAATAA ATAACATTTC
      GGAGAAAGGA ATAATTTGTA CATCTGATAT AGGTAAAAAA TGATTTTATT TATTGTAAAG

3361  AGATAATATC TTTGCACTGA TAATGTTGCC AAGCCATTTC TAAAGTGACC TTATCAATTT
      TCTATTATAG AAACGTGACT ATTACAACGG TTCGGTAAAG ATTTCACTGG AATAGTTAAA

3421  AATTACCATT GGATGAGGGT GTTGCTTTCA TCGCACCATT GTAGATTGTC TTTTTTATTT
      TTAATGGTAA CCTACTCCCA CAACGAAAGT AGCGTGGTAA CATCTAACAG AAAAAATAAA

3481  CAATTTGCGT TTATTTATAA CTGGTTGCAA AGGTACACAG AACACACGCT CCTTCAACTT
      GTTAAACGCA AATAAATATT GACCAACGTT TCCATGTGTC TTGTGTGCGA GGAAGTTGAA

3541  ATCTTTGATA AACCCAAGCA AGGATACAAA AAGTTGGACG ACATTGAGTA GAGTCATGGT
      TAGAAACTAT TTGGGTTCGT TCCTATGTTT TTCAACCTGC TGTAACTCAT CTCAGTACCA

3601  ATACGGTGCT GACCCTACAG TATCAGTGGA AAAGATAAGG AAAATGTCAC TACTCACCTA
      TATGCCACGA CTGGGATGTC ATAGTCACCT TTTCTATTCC TTTTACAGTG ATGAGTGGAT

3661  TGTTATGCAA AACAGTTAGG TGTGCTGGGG CTGGATACTG CTCTTTTACT TGAGCATTGG
      ACAATACGTT TTGTCAATCC ACACGACCCC GACCTATGAC GAGAAAATGA ACTCGTAACC

3721  TTGATTAAAG TTTAGGTACC ATCCAGGCTG GTCTAGAGAA GTCTTTGGAG TTAACCATGC
      AACTAATTTC AAATCCATGG TAGGTCCGAC CAGATCTCTT CAGAAACCTC AATTGGTACG

3781  TCTTTTTGTT AAAGAAGAGA GTAATGTGTT TATCCTGGCT CATAGTCCGT CACCGAAAAT
      AGAAAAACAA TTTCTTCTCT CATTACACAA ATAGGACCGA GTATCAGGCA GTGGCTTTTA

3841  AGAAAATGCC ATCCATAGGT AAAATGCTGA CCTATAGAAA AAAATGAACT CTACTTTTAT
      TCTTTTACGG TAGGTATCCA TTTTACGACT GGATATCTTT TTTTACTTGA GATGAAAATA

3901  AGCCTAGTAA AAATGCTCTA CCTGAGTAGT TAAAAGCAAT TCATGAAGCC TGAAGCTAAA
      TCGGATCATT TTTACGAGAT GGACTCATCA ATTTTCGTTA AGTACTTCGG ACTTCGATTT
```

FIG. 10A-4

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3961  GAGCACTCTG A. GTTTTGG CATAATAGCT GCATTTCCAG A. TGACCTT TGGCCCCAAC
      CTCGTGAGAC TACCAAAACC GTATTATCGA CGTAAAGGTC TGGACTGGAA ACCGGGGTTG

4021  CACAAGTGCT CCAAGCCCCA CCAGCTGACC AAAGAAAGCC CAAGTTCTCC TTCTGTCCTT
      GTGTTCACGA GGTTCGGGGT GGTCGACTGG TTTCTTTCGG GTTCAAGAGG AAGACAGGAA

4081  CCCACAACCT CCCTGCTCCC AAAACTATGA AATTAATTTG ACCATATTAA CACAGCTGAC
      GGGTGTTGGA GGGACGAGGG TTTTGATACT TTAATTAAAC TGGTATAATT GTGTCGACTG

4141  TCCTCCAGTT TACTTAAGGT AGAAAGAATG AGTTTACAAC AGATGAAAAT AAGTGCTTTG
      AGGAGGTCAA ATGAATTCCA TCTTTCTTAC TCAAATGTTG TCTACTTTTA TTCACGAAAC

4201  GGCGAACTGT ATTCCTTTTA ACAGATCCAA ACTATTTTAC ATTTAAAAAA AAAGTTAAAC
      CCGCTTGACA TAAGGAAAAT TGTCTAGGTT TGATAAAATG TAAATTTTTT TTTCAATTTG

4261  TAAACTTCTT TACTGCTGAT ATGTTTCCTG TATTCTAGAA AAATTTTTAC ACTTTCACAT
      ATTTGAAGAA ATGACGACTA TACAAAGGAC ATAAGATCTT TTTAAAAATG TGAAAGTGTA

4321  TATTTTTGTA CACTTTCCCC ATGTTAAGGG ATGATGGCTT TTATAAATGT GTATTCATTA
      ATAAAAACAT GTGAAAGGGG TACAATTCCC TACTACCGAA AATATTTACA CATAAGTAAT

4381  AATGTTACTT TAAAAATAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAA
      TTACAATGAA ATTTTTATTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTT
```

FIG. 10A-5

FIG. 10B

STEAP-2, AA508880 (NCI_CGAP Pr6)
ggtcgacttttcctttattcctttgtcagagatctgattcatccatatgctagaaaccaacagagtgacttttaca
aaattcctatagagattgtgaataaaaccttacctatagttgccattactttgctctccctagtataccttgcagg
tcttctggcagctgcttatcaactttattacggcaccaagtataggagatttccaccttggttggaaacctggtta
cagtgtagaaaacagcttggattactaagttgtttcttcgctatggtccatgttgcctacagcctctgcttaccga
tgagaaggtcagagagat (SEQ ID NO: 9)

STEAP-2, 98P4B6 SSH fragment
TTTGCAGCTTTGCAGATACCCAGACTGAGCTGGAACTGGAATTTGTCTTCCTATTGACTCTACTTCTTTAAAAGCG
GCTGCCCATTACATTCCTCAGCTGTCCTTGCAGTTAGGTGTACATGTGACTGAGTGTTGGCCAGTGAGATGAAGTC
TCCTCAAAGGAAGGCAGCATGTGTCCTTTTT (SEQ ID NO: 10)

STEAP-3, AI139607 (testis EST)
aagaaggagaatccatttagcacctcctcagcctggctcagtgattcatatgtggctttgggaatacttgggtttt
ttctgtttgtactcttgggaatcacttctttgccatctgttagcaatgcagtcaactggagagagttccgatttgt
ccagtccaaactgggttatttgaccctgatcttgtgtacagcccacaccctggtgtacggtgggaagagattcctc
agcccttcaaatctcagatggtatcttcctgcagcctacgtgttagggcttatcattccttgcactgtgctggtga
tcaagtttgtcctaatcatgccatgtgtagacaacacccttacaaggatccgccagggctgggaaaggaactcaaa
acactagaaaaagcattgaatggaaaatcaatatttaaaacaaagttcaatttagctggaaaaaaaaa
(SEQ ID NO: 11)

STEAP 4, R80991 (placental EST)
ggccgcggcanccgctacgacctggtcaacctggcagtcaagcaggtcttggccanacaagagccacctctgggtg
aaggaggaggtctggcggatggagatctacctctccctgggagtgctggccctcggcacgttgtccctgctggccg
tgacctcactgccgtccattgcaaactcgctcaactggagggagttcagcttcgttcagtcctcactgggctttgt
ggccntcgtgctgagcacactncacacgctcacctacggctggacccgcgccttcgaggagagccgctacaagttc
tacctncctcccaccttcacgntcacgctgctggtgccctgcgttcgttcatcctgggccaaagccctgtttntac
tgccttgcattcagccgnaga (SEQ ID NO: 12)

FIG. 11A-1

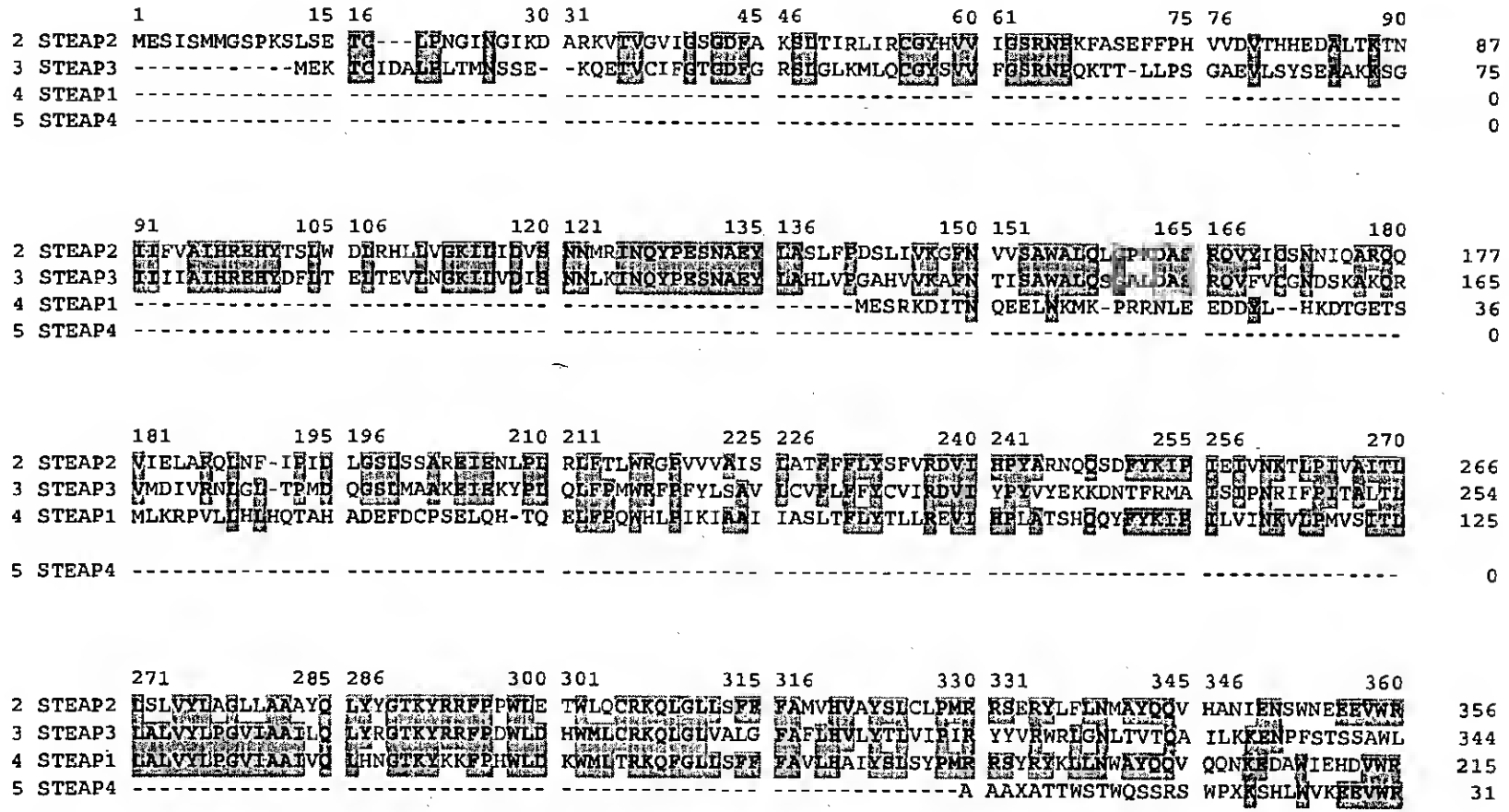

FIG. 11A-2

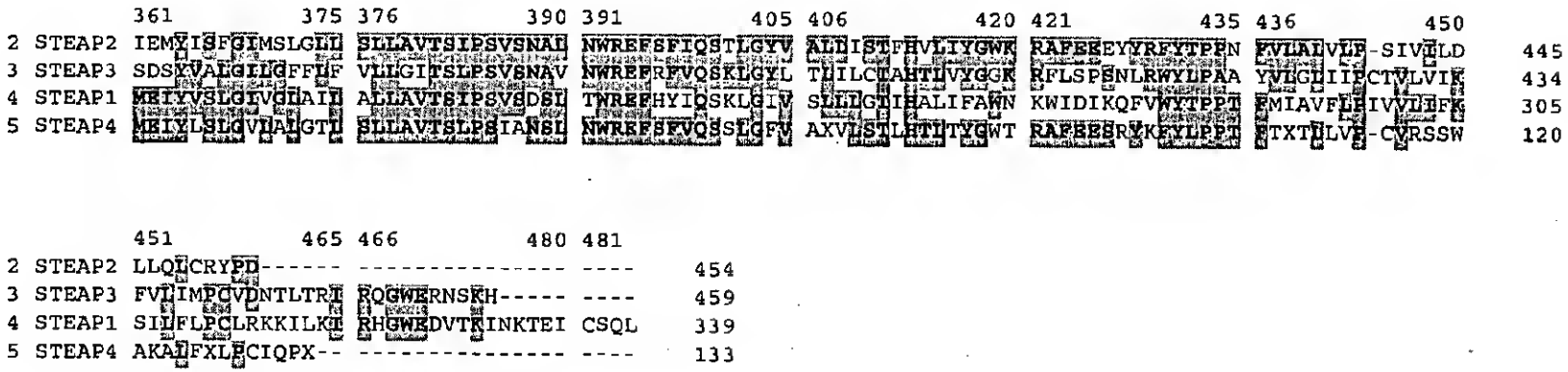
361 375 376 390 391 405 406 420 421 435 436 450
2 STEAP2 IEMYISFGIMSLGLL SLLAVTSIPSVSNAL NWREFSFIQSTLGYV ALDISTFHVLIYGWK RAFEEEYYRFYTPPN FVLALVLP-SIVILD 445
3 STEAP3 SDSKVALGILGFFIF VLLGITSLPSVSNAV NWREFRFVQSKLGYL THILCLAHTLVYGGK RFLSPSNLRWYLPAA YVLGLIIFCTVLVIK 434
4 STEAP1 MEIVVSLGIVGILAIL ALLAVTSIPSVSDSL TWREFHYIQSKLGIV SLLLGTIHALIFAWN KWIDIKQFVWYTPPT FMIAVFLPIVVLEFK 305
5 STEAP4 MEIYLSLGVLALGTL SLLAVTSLPSIANSL NWREFSFVQSSLGFV AXVLSTLHTLTYGWT RAFEEERYKEYLPPT FTXTILVF-CVRSSW 120
451 465 466 480 481
2 STEAP2 LLQLCRYPD------ ---------- ---- 454
3 STEAP3 FVLIMPCVDNTLTRI RQGWERNSKH----- ---- 459
4 STEAP1 SILFLPCLRKKILKT RHGWEDVTKINKTEI CSQL 339
5 STEAP4 AKALFXLPCIQPX-- ---------- ---- 133

FIG. 11B

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STRAP-1     67 LFPQWHLPIKIAAIIASLTFLYTLLREVIHPLATSHQQYFYKIPILVINKVLPMVSITLL
STRAP-2    208 LFTLWRGPVVVAISLATFFFLYSFVRDVIHPYARNQQSDFYKIPIEIVNKTLPIVAITLL
               **  *  *   *   *   ***   * **** *   *  ******   ** ** * ****

STRAP-1    127 ALVYLPGVIAAIVQLHNGTKYKKFPHWLDKWMLTRKQFGLLSFFFAVLHAIYSLSYPMRR
STRAP-2    268 SLVYLAGLLAAAYQLYYGTKYRRFPPWLETWLQCRKQLGLLSFFFAMVHVAYSLCLPMRR
                **** *  **  **  ****  ** **  *   *** ********  *  ***  ****

STRAP-1    187 SYRYKLLNWAYQQVQQNKEDAWIEHDVWRMEIYVSLGIVGLAILALLAVTSIPSVSDSLT
STRAP-2    328 SERYLFLNMAYQQVHANIENSWNEEEVWRIEMYISFGIMSLGLLSLLAVTSIPSVSNALN
               * **  ** *****  * *  * *  *** * * * **  *  * ***********  *

STRAP-1    247 WREFHYIQSKLGIVSLLLGTIHALIFAWNKWIDIKQFVWYTPPTFMIAVFLPIVVLI
STRAP-2    388 WREFSFIQSTLGYVALLISTFHVLIYGWKRAFEEEYYRFYTPPNFVLALVLPSIVIL
               ****  *** ** * **  * * **  *          **** *  *  **  *
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FIG. 11C

```
STEAP1  66 ELFPQWHLPIKIAAIIASLTFLYTLLREVIHPLATSHQQYFYKIPILVINKVLPMVSITL

STEAP3 195 QLFPMWRFPFYLSAVLCVFLFFYCVIRDVIYPYVYEKKDNTFRMAISIPNRIFPITALTL
            *** *  *    *      * *   * ** *             *   *   *    **

STEAP1 126 LALVYLPGVIAAIVQLHNGTKYKKFPHWLDKWMLTRKQFGLLSFFFAVLHAIYSLSYPMR

STEAP3 255 LALVYLPGVIAAILQLYRGTKYRRFPDWLDHWMLCRKQLGLVALGFAFLHVLYTLVIPIR
           ************** **  ****  ** *** *** *** **    ** **  * *  * *

STEAP1 186 RSYRYKLLNWAYQQVQQNKEDAWIEHDVWRMEIYVSLGIVGLAILALLAVTSIPSVSDSL

STEAP3 315 YYVRWRLGNLTVTQAILKKENPFSTSSAWLSDSYVALGILGFFLFVLLGITSLPSVSNAV
              *  * *    *    **        *    ** *** *     **  ** ****

STEAP1 246 TWREFHYIQSKLGIVSLLLGTIHALIFAWNKWIDIKQFVWYTPPTFMIAVFLPIVVLIFK

STEAP3 375 NWREFRFVQSKLGYLTLILCTAHTLVYGGKRFLSPSNLRWYLPAAYVLGLIIPCTVLVIK
            ****   *****   * * * * *              ** *         *  **  *

STEAP1 306 SILFLPCLRKKILKIRHGWEDVTK

STEAP3 435 FVLIMPCVDNTLTRIRQGWERNSK
            *  **       ** ***   *
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FIG. 11D

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STEAP2   29 RKVTVGVIGSGDFAKSLTIRLIRCGYHVVIGSRNPKFASEFFPHVVDVTHHEDALTKTNI

STEAP3   18 KQETVCIFGTGDFGRSLGLKMLQCGYSVVFGSRNPQ-KTTLLPSGAEVLSYSEAAKKSGI
               **   * ***  **      *** ** *****       *    *     *  *  *


STEAP2   89 IFVAIHREHYTSLWDLRHLLVGKILIDVSNNMRINQYPESNAEYLASLFPDSLIVKGFNV

STEAP3   77 IIIAIHREHYDFLTELTEVLNGKILVDISNNLKINQYPESNAEYLAHLVPGAHVVKAFNT
            *  *******  *  *   * **** * ***  ************* * *    ** **


STEAP2  149 VSAWALQLGPKDASRQVYICSNNIQARQQVIELARQLNFIPIDLGSLSSAREIENLPLRL

STEAP3  137 ISAWALQSGALDASRQVFVCGNDSKAKQRVMDIVRNLGLTPMDQGSLMAAKEIEKYPLQL
             ****** *  ******  * *   * * *    * *   * * ***  * ***  ** *


STEAP2  209 FTLWRGPVVVAISLATFFFLYSFVRDVIHPYARNQQSDFYKIPIEIVNKTLPIVAITLLS

STEAP3  197 FPMWRFPFYLSAVLCVFLFFYCVIRDVIYPYVYEKKDNTFRMAISIPNRIFPITALTLLA
            *  ** *      *  * * *   **** **            * * *   ** * ***


STEAP2  269 LVYLAGLLAAAYQLYYGTKYRRFPPWLETWLQCRKQLGLLSFFFAMVHVAYSLCLPMRRS

STEAP3  257 LVYLPGVIAAILQLYRGTKYRRFPDWLDHWMLCRKQLGLVALGFAFLHVLYTLVIPIRYY
            **** *  **  *** ******** **  *  *******    **  ** * *  * *


STEAP2  329 ERYLFLNMAYQQVHANIENSWNEEEVWRIEMYISFGIMSLGLLSLLAVTSIPSVSNALNW

STEAP3  317 VRWRLGNLTVTQAILKKENPFSTSSAWLSDSYVALGILGFFLFVLLGITSLPSVSNAVNW
             *    *    *     **       *    *   **    *  **  ** ****** **


STEAP2  389 REFSFIQSTLGYVALLISTFHVLIYGWKRAFEEEYYRFYTPPNFVLALVLPSIVIL

STEAP3  377 REFRFVQSKLGYLTLILCTAHTLVYGGKRFLSPSNLRWYLPAAYVLGLIIPCTVLV
            *** * ** ***  *   * * * ** **       * * *   ** *  *  *
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